

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 30, 2004, 14:21:47 ; Search time 93.3333 Seconds
(without alignments)
38.435 Million cell updates/sec

Title: US-10-046-922-35

Perfect score: 72

Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 202273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0

<Maximum-DB-seq-length: 10>

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003s:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 72 | 100.0 | 10 | 5 | ABP53932 |
| 2 | 54 | 75.0 | 10 | 5 | ABP53931 |
| 3 | 50 | 69.4 | 10 | 5 | ABP53968 |
| 4 | 39.5 | 54.9 | 9 | 5 | ABJ04472 |
| 5 | 35.5 | 49.3 | 9 | 5 | ABJ04461 |
| 6 | 35 | 48.6 | 9 | 5 | ABJ04460 |
| 7 | 33.5 | 46.5 | 7 | 5 | ABJ04531 |
| 8 | 33 | 45.8 | 7 | 5 | ABP53964 |
| 9 | 33 | 45.8 | 8 | 2 | AAV03715 |
| 10 | 33 | 45.8 | 8 | 3 | AAV76817 |
| 11 | 33 | 45.8 | 8 | 5 | ABP53965 |
| 12 | 33 | 45.8 | 8 | 7 | ADG94005 |
| 13 | 33 | 45.8 | 8 | 8 | ADL98014 |
| 14 | 33 | 45.8 | 10 | 5 | ABB46346 |
| 15 | 33 | 45.8 | 10 | 5 | ABB46607 |
| 16 | 32 | 44.4 | 7 | 3 | AAV76794 |
| 17 | 32 | 44.4 | 7 | 5 | ABP53418 |
| 18 | 32 | 44.4 | 9 | 4 | ABP22609 |
| 19 | 32 | 44.4 | 9 | 4 | ABP20314 |
| 20 | 32 | 44.4 | 9 | 5 | AAU90543 |
| 21 | 32 | 44.4 | 9 | 5 | AAU90464 |
| 22 | 32 | 44.4 | 9 | 5 | AAU90542 |
| 23 | 32 | 44.4 | 9 | 5 | AAU90541 |
| 24 | 32 | 44.4 | 10 | 2 | AAW43886 |
| 25 | 32 | 44.4 | 10 | 3 | AAV66209 |

| | | | | | |
|----|------|------|----|---|----------|
| 26 | 32 | 44.4 | 10 | 3 | AAV66213 |
| 27 | 32 | 44.4 | 10 | 4 | ABP20316 |
| 28 | 32 | 44.4 | 10 | 4 | ABP20318 |
| 29 | 32 | 44.4 | 10 | 4 | ABP22613 |
| 30 | 32 | 44.4 | 10 | 4 | ABP14381 |
| 31 | 32 | 44.4 | 10 | 4 | ABP22611 |
| 32 | 32 | 44.4 | 10 | 5 | AAU88395 |
| 33 | 32 | 44.4 | 10 | 5 | AAU90462 |
| 34 | 32 | 44.4 | 10 | 5 | AAU90463 |
| 35 | 32 | 44.4 | 10 | 5 | AAU90535 |
| 36 | 32 | 44.4 | 10 | 8 | ADG64384 |
| 37 | 32 | 44.4 | 10 | 8 | ADH58622 |
| 38 | 31 | 43.1 | 8 | 2 | AAW97529 |
| 39 | 31 | 43.1 | 9 | 5 | ABP53933 |
| 40 | 31 | 43.1 | 9 | 5 | ABJ04488 |
| 41 | 31 | 43.1 | 9 | 8 | ADN64476 |
| 42 | 31 | 43.1 | 10 | 4 | AAU95260 |
| 43 | 30.5 | 42.4 | 10 | 2 | AAU14709 |
| 44 | 30 | 41.7 | 8 | 2 | AAW12859 |
| 45 | 30 | 41.7 | 8 | 3 | AAV91924 |

ALIGNMENTS

RESULT 1

ABP53932

ID ABP53932 standard; peptide; 10 AA.

XX AC ABP53932;

XX DT 09-JAN-2003 (first entry)

XX DE VEGFR-3 binding peptide SEQ ID NO:35.

XX KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
 KW cytosolic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
 KW lymphatic; cell surface receptor; cancer; neovascularisation;
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
 KW diabetes; PDGF; platelet derived growth factor.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200257299-A2.

XX PD 25-JUL-2002.

XX PF 16-JAN-2002; 2002WO-IB000099.

XX PR 17-JAN-2001; 2001US-0262476P.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PP (LICN) LICENTIA LTD.

XX PI Alitalo K, Koivunen E, Kubo H;

XX DR WPI; 2002-691521/74.

XX PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
 diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
 such as cancer and diseases of neovascularization.

XX PS Claim 13; Page 80; 149pp; English.

XX CC The present invention describes an isolated peptide (I) that binds to and
 inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
 have cytostatic, hepatotropic, antiinflammatory, hypotensive,
 antidiabetic and vulnary activities, and can be used in gene therapy.
 CC Compositions and methods from the present invention are useful for
 diagnosing, evaluating and treating disorders mediated by the activity of
 the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 72; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
| | | | |
Db 1 CGYWLTIWGC 10

RESULT 2
ABP53931
ID ABP53931 standard; peptide; 10 AA.
XX
AC ABP53931;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:34.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytosolic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnary; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
FH Misc-difference 1 /note= "any amino acid"
FT Misc-difference 10 /note= "any amino acid"
FT Misc-difference 10 /note= "any amino acid"
XX
PN WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB0000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX
DR WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Claim 12; Page 80; 149pp; English.

CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 10 AA;

Query Match 75.0%; Score 54; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9
| | | | |
Db 2 GYWLTIWG 9

RESULT 3
ABP53968
ID ABP53968 standard; peptide; 10 AA.
XX
AC ABP53968;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:73.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytosolic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnary; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
FH Misc-difference 5.7 /note= "X is any amino acid"
FT Misc-difference 9 /note= "X is any amino acid"
FT Misc-difference 9 /note= "X is any amino acid"
XX
PN WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB0000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX
DR WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Disclosure; Page 147; 149pp; English.

CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a VSGPR-3 binding peptide, which is given in the
CC exemplification of the present invention

Sequence 10 AA;

Query Match 69.4%; Score 50; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 4; Indels

Qy 1 CGYWLTIWGC 10
||| |
Db 1 CGYWXXXWXC 10

RESULT 4
ABJ04472
ID ABJ04472 standard: peptide: 9 AA.

AC ABJ04472;

24-OCT-2002 (first entry)

xx Stem cell (mesenchymal) targeting peptide 61.

KW
XX
BRASIL; targeting peptide; bacterial infection;

KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
 KW antibody; targeting peptide; bacterial infection;
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
 KW viral infection; cardiovascular disease; degenerative disease.

xx OS Unidentified.

AA
PN
WO200220822-A2.14-MAR-2002.
PD
AA

07-SEP-2001; 2001WO-US028124.

PR 08-SEP-2000; 2000US-0231266P.

XX
T0159/00-301007; T007-NW0-1T Y3

FA 1 YEAR / ONLY TEXAS SYSTEM.
XX

XX
 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 26

XX
DK
WFT; 2007/09/11

PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
PT of Selective Ligands) method comprises a single differential
PT centrifugation step.

PS Example 5; Page 76; 167pp; English.

The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as: diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardiovascular disease and degenerative disease. The present amino acid sequence represents a

CC targeting peptide of the invention
XX
SQ Sequence 9 AA:

Query Match 54.9%; Score 39.5; DB 5; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 2; Indels

Qy 1 CGYWLTIWGC 10

Db 1 CG-WFSWWGC 9

RESOL 3
ABJ04461

ID ABJ04461 standard; peptide; 9 AA.

AC ABJ04461;

DT 24-OCT-2002 (first entry)

DE Stem cell (mesenchymal) targeting peptide 50.

KW BRASIL; targeting peptide; bacterial infection;

inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; viral infection; cardiovascular disease; degenerative disease.

OS Unidentified.

PN WO200220822-A2.

PD 14-MAR-2002.

PF 07-SEP-2001; 2001WO-US028124.

PR 08-SEP-2000; 2000US-0231266P.

XX
T07C9/A0-COT00Z / T00Z-NAO-IT VJ

XX
STATISTICS / UNIT 10XX
XXXX
XX
CE/COFO-2007, ITM

PT of Selective Ligands) method comprises a single differential centrifugation step.

PS Example 5; Page 76; 167pp; English.

The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as: diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardiovascular disease and degenerative disease. The present amino acid sequence represents a targeting peptide of the invention.

Sequence 9 AA; SQ

Query Match 49.3%; Score 35.5; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWLTIWGC 10
 ||:|:|
 Db 1 CGWW-GLWPC 9

RESULT 6
 ABJ04460
 ID ABJ04460 standard; peptide; 9 AA.

XX AC ABJ04460;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Stem cell (mesenchymal) targeting peptide 49.
 XX
 KW BRASIL; targeting peptide; bacterial infection;
 KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
 KW viral infection; cardiovascular disease; degenerative disease.

XX Unidentified.

XX WO200220822-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028124.

XX 08-SEP-2000; 2000US-0231266P.

XX 17-JAN-2001; 2001US-00765101.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-404697/43.

XX Identification of targeting peptides that can be used to treat diseases
 e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
 of Selective Ligands) method comprises a single differential
 centrifugation step.

PS Example 5; Page 76; 167pp; English.

XX The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 of Selective Interactive Ligands) to obtain a targeting peptide. The
 BRASIL method of the invention involves: exposing a target to a phage
 display library in a first phase; exposing the first phase to a second
 phase; and separating the phage bound to the target from unbound phage.
 The BRASIL method of the invention allows cell phages to be separated
 from the remaining unbound phage in a single differential centrifugation
 step. When compared to conventional cell panning methods, the BRASIL
 method shows a significant increase in recovery of specific phage and a
 substantial decrease in background. The BRASIL method is useful for
 identifying targeting peptides. The targeting peptides identified by the
 method of the invention are useful for treating disease states, such as:
 diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 disease; bacterial infection; viral infection; cardiovascular disease and
 degenerative disease. The present amino acid sequence represents a
 targeting peptide of the invention

XX Sequence 9 AA;

Query Match 48.6%; Score 35; DB 5; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGYWLTIW 8
 ||:|:|
 Db 1 CDWWTAW 8

RESULT 7

ABJ04531
 ID ABJ04531 standard; peptide; 7 AA.

XX AC ABJ04531;

XX 24-OCT-2002 (first entry)

XX Molt-4 leukaemia cell line targeting peptide 16.

XX BRASIL; targeting peptide; bacterial infection;
 KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
 KW viral infection; cardiovascular disease; degenerative disease.

XX Unidentified.

XX WO200220822-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028124.

XX 08-SEP-2000; 2000US-0231266P.

XX 17-JAN-2001; 2001US-00765101.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-404697/43.

XX Identification of targeting peptides that can be used to treat diseases
 e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
 of Selective Ligands) method comprises a single differential
 centrifugation step.

XX Claim 79; Page 100; 167pp; English.

XX The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 of Selective Interactive Ligands) to obtain a targeting peptide. The
 BRASIL method of the invention involves: exposing a target to a phage
 display library in a first phase; exposing the first phase to a second
 phase; and separating the phage bound to the target from unbound phage.
 The BRASIL method of the invention allows cell phages to be separated
 from the remaining unbound phage in a single differential centrifugation
 step. When compared to conventional cell panning methods, the BRASIL
 method shows a significant increase in recovery of specific phage and a
 substantial decrease in background. The BRASIL method is useful for
 identifying targeting peptides. The targeting peptides identified by the
 method of the invention are useful for treating disease states, such as:
 diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 disease; bacterial infection; viral infection; cardiovascular disease and
 degenerative disease. The present amino acid sequence represents a
 targeting peptide of the invention

XX Sequence 7 AA;

Query Match 46.5%; Score 33.5; DB 5; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

Qy 1 CGYWLTIWGC 10

Db 1 CSVW---WGC 7

RESULT 8

ABP53964
 ID ABP53964 standard; peptide; 7 AA.

XX AC ABP53964;

XX DT 09-JAN-2003 (first entry)
 XX DE VEGFR-3 binding peptide SEQ ID NO:67.
 XX KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
 XX KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
 KW vulnary; cell surface receptor; cancer; neovascularisation;
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
 KW diabetes; PDGF; platelet derived growth factor.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 4..6 /note= "X is any amino acid"
 FT WO200257299-A2.
 PN 25-JUL-2002.
 XX 16-JAN-2002; 2002WO-IB0000099.
 XX 17-JAN-2001; 2001US-0262476P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 XX Alltalo K, Koivunen E, Kubo H;
 PI WPI; 2002-691521/74.
 DR New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
 PT such as cancer and diseases of neovascularization.
 XX Claim 21; Page 81; 149pp; English.
 PS The present invention describes an isolated peptide (I) that binds to and
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
 CC antidiabetic and vulnary activities, and can be used in gene therapy.
 CC Compositions and methods from the present invention are useful for
 CC diagnosing, evaluating and treating disorders mediated by the activity of
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence
 CC represents a specifically claimed VEGFR-3 binding peptide from the
 CC present invention
 XX Sequence 7 AA;
 SQ
 Query Match 45.8%; Score 33; DB 5; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GYWLTIW 8
 |||||
 Db 1 GYWXXXW 7
 RESULT 9
 AAY03715
 ID AAY03715 standard; peptide; 8 AA.
 XX AC AAY03715;
 XX DT 08-JUN-1999 (first entry)

XX DE Fluorine-18 (F-18) labeled peptide 2.
 XX KW 18F radionuclide; targeting vector; positron emission tomography; F-18;
 KW radiolabeling; thiol; fluorine-18.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "N-terminal acetylation; optionally has a free or
 FT protected thiol group"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue; optionally has a free or
 FT protected thiol group"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 8 /note= "D-form residue"
 FT WO9911590-A1.
 PN 11-MAR-1999.
 XX 03-SEP-1998; 98WO-US018268.
 PF 03-SEP-1997; 97US-0057485P.
 PR (IMMU-) IMMUNOMEDICS INC.
 PA Griffiths GL;
 PI WPI; 1999-228967/19.
 DR Radiolabeling thiol-containing peptides with fluorine-18.
 XX Claim 14; Page 15; 22pp; English.
 PS The invention relates to a method for incorporating 18F radionuclide into
 CC peptide-containing targeting vectors for use in clinical positron
 CC emission tomography. Radiolabeling thiol-containing peptides with
 CC fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol
 CC group with a labeling reagent of formula: 18F-(CH₂)_m-CR1R2-(CH₂)_n-X, or a
 CC fluorinated alkene in which at least one of the two double bonded carbon
 CC atoms bears at least one leaving group comprising I, Br, Cl, azide,
 CC tosylate, mesylate, nosylate or triflate. n, m = 0-2; n+m = 0-2; X = I,
 CC Br, Cl, azide, tosylate, mesylate, nosylate, triflate, maleimide
 CC (optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; R1, R2 = I,
 CC Br, Cl, azide, tosylate, mesylate, nosylate, triflate, H, CONH2, COOH,
 CC OH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl (optionally
 CC substituted by CONH2, COOH, OH, sulfonic acid, tertiary amine or
 CC quaternary ammonium), COOR', CONR'2 or COR'; and R' = 1-6C alkyl or
 CC phenyl. The method is used for Radiolabeling peptide-containing targeting
 CC vectors such as proteins, antibodies, antibody fragments and receptor-
 CC targeted peptides for use in routine clinical positron emission
 CC tomography. The method is simple and efficient. The method uses the
 CC unique property of the free thiol groups which are rapidly alkylated at
 CC neutral pH and moderate temperature. Sequences AAY03714-716 represent
 CC examples of F-18 labeled peptides used in the method of detecting a
 CC tissue
 XX Sequence 8 AA;
 SQ
 Query Match 45.8%; Score 33; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGYW 4
 |||||

Query Match 45.8%; Score 33; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
DB 1 GIWXXXW 7

RESULT 12
ADG94005
ID ADG94005 standard; peptide; 8 AA.
AC ADG94005;
DT 11-MAR-2004 (first entry)
XX Immunogenic peptide.
XX Immunogenic peptide; multi-specific antibody; polymer conjugate; tumour;
KW cytostatic; photodynamic therapy.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Optionally methylated or Acetylated"
FT Misc-difference 2
FT /note= "D-form residue"
FT Misc-difference 3
FT /note= "D-form residue"
FT Misc-difference 5
FT /note= "Optionally methylated or Acetylated D-form residue"
FT Misc-difference 7
FT /note= "D-form residue"
FT Misc-difference 8
FT /note= "D-form residue"
XX US2003026764-A1.
XX
XX
XX
XX 06-FEB-2003.
XX 31-JUL-2002; 2002US-00209592.
XX 31-JUL-2001; 2001US-0308605P.
XX (IMMU-) IMMUNOMEDICS INC.
XX Griffiths GL;
XX WPI; 2003-801085/75.
XX Targeting an agent towards a target site in a tissue, by administering in
PT a tissue, a multi-specific antibody or its fragment and a polymer
PT conjugate that binds to the capture arm of the multi-specific antibody.
XX Disclosure; Page 14; 19pp; English.
XX The invention relates to targeting an agent towards a target site in a
CC tissue, comprising administering to the tissue, a multi-specific antibody
CC or its fragment, comprising a targeting arm that binds to an antigen of
CC the target site and a capture arm that binds to a polymer conjugate, and
CC administering a polymer conjugate that binds to the capture arm, the
CC conjugate has a polymer conjugated to the agent such as therapeutic
CC agent, a peptide, an enzyme and a labelled ligand. Also included is a kit
CC useful for targeting a target site within a tissue in a subject or tissue
CC sample comprising the above mentioned multi-specific antibody or its
CC fragment and a polymer conjugate. The method is used for targeting an
CC agent towards a target site in a tissue (e.g. a tumour). The method is
CC also useful for therapeutic or diagnostic purposes and further in
CC photodynamic therapy. The present sequence is an immunogenic peptide used

CC in the method of the invention.
XX Sequence 8 AA;
SQ Query Match 45.8%; Score 33; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYW 4
DB 5 CGYW 8

RESULT 13
ADL98014
ID ADL98014 standard; peptide; 8 AA.
XX
XX ADL98014;
AC ADL98014;
DT 20-MAY-2004 (first entry)
XX Peptide hapten #2.
XX
XX photodynamic diagnosis; cancer; tumour; cardiovascular lesion;
KW inflammatory disease; neurodegenerative disease; metabolic disease;
KW infectious disease; B-cell malignancy; Alzheimer's disease; amyloidosis;
KW autoimmune disease; bacterial infection; fungal infection;
KW parasitic infection; viral infection;
KW carcinoembryonic antigen-expressing tumour.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Optionally Cysteinylyl; if Cys the residue is
FT methylated; N-terminal acetylated."
FT Misc-difference 2
FT /note= "D form residue"
FT Misc-difference 3
FT /note= "D form residue"
FT Modified-site 5
FT /note= "Optionally Cysteinylyl; if Cys the residue is
FT methylated; N-terminal acetylated."
FT Misc-difference 7
FT /note= "D form residue"
FT Misc-difference 8
FT /note= "D form residue"
XX US2004043030-A1.
XX
XX 04-MAR-2004.
XX 09-JUN-2003; 2003US-00456580.
XX 31-JUL-2001; 2001US-0308605P.
PR 31-JUL-2002; 2002US-00209592.
XX (IMMU-) IMMUNOMEDICS INC.
XX Griffiths GL, Goldenberg DM, Hansen HJ;
XX WPI; 2004-313738/29.
XX Treating cancer and metabolic diseases by administering a multi-specific
PT antibody having a targeting arm that binds to an antigen and a capture
PT arm that binds to a polymer conjugate comprising a therapeutic agent.
XX Disclosure; Page 16; 24pp; English.
XX The invention relates to a method of diagnosing or treating a disease or
CC disorder. The method involves administering to a tissue a multi-specific
CC antibody (I) or antibody fragment, comprising a targeting arm that binds
CC to an antigen on the target site, and a capture arm that binds to a

CC polymer conjugate, and administering to the tissue a polymer conjugate
 CC that binds to the capture arm, the polymer conjugate comprising a polymer
 CC conjugated to a diagnostic or therapeutic agent. Also included is a
 CC method for photodynamic diagnosis or treatment of a disease or disorder;
 CC or intravascular or endoscopic method for diagnosing or treating a
 CC disease or disorder. The method is useful for diagnosing or treating a
 CC disease or disorder chosen from cancer (oesophageal, gastric, colonic,
 CC rectal, pancreatic, lung, breast, ovarian, urinary bladder, endometrial,
 CC cervical, testicular, renal, adrenal and liver cancer, solid tumour, B-
 CC cell malignancy or T-cell malignancy); cardiovascular lesion; an
 CC inflammatory disease; neurodegenerative disease; metabolic disease; and
 CC an infectious disease. The B-cell malignancy is chosen from indolent
 CC forms of B-cell lymphomas, aggressive forms of B-cell lymphomas, chronic
 CC lymphatic leukaemias, acute lymphatic leukaemias, and multiple myeloma.
 CC The solid tumour is chosen melanoma, carcinoma (preferably renal
 CC carcinoma, lung carcinoma, intestinal carcinoma, and stomach carcinoma),
 CC glioma and sarcoma. The cardiovascular lesion is chosen from infarct,
 CC clot, embolus, atherosclerotic plaque and ischaemia. The
 CC neurodegenerative disease is Alzheimer's disease. The metabolic disease
 CC is amyloidosis, where the antibody binds amyloid. The disease or disorder
 CC is displaced or ectopic normal tissue chosen from endometrium, thymus,
 CC spleen and parathyroid. The method can be used for normal tissue
 CC ablation, where the tissue is chosen from bone marrow and spleen. The
 CC disease or disorder is an autoimmune disease such as myasthenia gravis,
 CC lupus nephritis, lupus erythematosus, and rheumatoid arthritis. Class III
 CC autoimmune diseases such as immune-mediated thrombocytopenias, such as
 CC acute idiopathic thrombocytopenic purpura and chronic idiopathic
 CC thrombocytopenic purpura, dermatomyositis, Sjogren's syndrome, multiple
 CC sclerosis, Sydenham's chorea, myasthenia gravis, systemic lupus
 CC erythematosus, lupus nephritis, rheumatic fever, polyglandular syndromes,
 CC bullous pemphigoid, diabetes mellitus, Henoch-Schönlein purpura, post-
 CC streptococcal nephritis, erythema nodosum, Takayasu's arteritis, colitis,
 CC Addison's disease, rheumatoid arthritis, sarcoidosis, ulcerative colitis,
 CC erythema multiforme, IgA nephropathy, polyarthritis nodosa, ankylosing
 CC spondylitis, Goodpasture's syndrome, thromboangiitis obliterans, primary
 CC biliary cirrhosis, Hashimoto's thyroiditis, thyrotoxicosis, scleroderma,
 CC chronic active hepatitis, polymyositis/dermatomyositis, polychondritis,
 CC pemphigus vulgaris, Wegener's granulomatosis, membranous nephropathy,
 CC ankyrotrophic lateral sclerosis, tabes dorsalis, Giant cell
 CC arteritis/polyvalgia, pernicious anaemia, rapidly progressive
 CC glomerulonephritis, or fibrosing alveolitis. The infectious disease is
 CC chosen from bacterial, fungal, parasitic and viral lesion. The infectious
 CC disease is caused by a fungus chosen from Microsporium, Trichophyton,
 CC Epidermophyton, Sporothrix schenckii, Cryptococcus neoformans,
 CC Coccidioides immitis, Histoplasma capsulatum, Blastomycosis dermatitidis,
 CC and Candida albicans. The infectious disease is caused by a virus chosen
 CC from HIV, herpes virus, cytomegalovirus, rabies virus, influenza virus,
 CC hepatitis B virus, Sendai virus, feline leukemia virus, Reo virus, polio
 CC virus, human serum parvo-like virus, simian virus 40, respiratory
 CC syncytial virus, mouse mammary tumour virus, Varicella-Zoster virus,
 CC Dengue virus, rubella virus, measles virus, adenovirus, human T-cell
 CC leukemia viruses, Epstein-Barr virus, murine leukemia virus, mumps virus,
 CC vesicular stomatitis virus, Sindbis virus, lymphocytic choriomeningitis
 CC virus, wart virus and blue tongue virus. The infectious disease is caused
 CC by a bacterium chosen from Bacillus anthracis, Streptococcus agalactiae,
 CC Legionella pneumophila, Streptococcus pyogenes, Escherichia coli,
 CC Neisseria gonorrhoeae, Neisseria meningitidis, Pneumococcus, Haemophilus
 CC influenzae B, Treponema pallidum, Lyme disease spirochetes, Pseudomonas
 CC aeruginosa, Mycobacterium leprae, Brucella abortus, Mycobacterium
 CC tuberculosis, and Tetanus toxin. The infectious disease is caused by a
 CC protozoa chosen from Plasmodium falciparum, Plasmodium vivax, Toxoplasma
 CC gondii, Trypanosoma rangeli, Trypanosoma cruzi, Trypanosoma
 CC rhodesiense, Trypanosoma brucei, Schistosoma mansoni, Schistosoma
 CC japonicum, Babesia bovis, Elmeria tenella, Onchocerca volvulus,
 CC Leishmania tropica, Trichinella spiralis, Onchocerca volvulus, Theileria
 CC parva, Taenia hydatigena, Taenia ovis, Taenia saginata, Echinococcus
 CC granulosus, and Mesocostoides corti. The infectious disease is caused by
 CC a mycoplasma chosen from Mycoplasma arthritidis, M. hyorhinis, M. orale,
 CC M. arginini, Acholeplasma laidlawii, M. salivarium, M. pneumoniae. The
 CC cancer is preferably chosen from carcinoembryonic antigen (CEA)-
 CC expressing tumour or a CD20-expressing malignancy. The present sequence
 CC represents a peptide used in the method of the invention.

SQ Sequence 8 AA;
 Query Match 45.8%; Score 33; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGYW 4
 DB 5 CGYW 8
 RESULT 14
 ABB46346
 ID ABB46346 standard; peptide; 10 AA.
 XX
 AC ABB46346;
 DT 30-JAN-2002 (first entry)
 XX
 DE Desmoglein-2 CAR sequence cyclic peptide SEQ ID NO 1090.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KM cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
 XX
 OS Synthetic.
 XX
 PN W0200172956-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-IB001400.
 XX
 PR 27-MAR-2000; 2000US-00535852.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI; 2002-025778/03.
 DR
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.
 XX
 PS Claim 18; Page 101; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.
 CC carcinoma, leukaemia or melanoma) and induce apoptosis
 XX
 SQ Sequence 10 AA;
 Query Match 45.8%; Score 33; DB 5; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CGYWLITWGC 10
 DB 1 CGYALDARGC 10
 RESULT 15

ABB46607
ID ABB46607 standard; peptide; 10 AA.
XX
AC ABB46607;
XX
DT 30-JAN-2002 (first entry)
XX
DE Desmocollin-1 CAR cyclic peptide 9.
XX
KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
XX
OS Synthetic.
XX
XX WO200172956-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001WO-IB001400.
XX
XX 27-MAR-2000; 2000US-00535852.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk OW, Symonds JM, Gour BJ;
XX
XX WPI; 2002-025778/03.
XX
XX Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX
XX Claim 23; Page 109; 127pp; English.
XX
XX The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polynucleotide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer (e.g.
CC carcinoma, leukaemia or melanoma) and induce apoptosis
XX
SQ Sequence 10 AA;

Query Match 45.8%; Score 33; DB 5; Length 10;
Best Local Similarity 60.0%; Pred.No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
||| |
Db 1 CGYATTADGC 10

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Job time : 103.333 secs

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OM protein - protein search, using sw model

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Title: US-10-046-922-35

Perfect score: 72

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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| 1 | 33 | 45.8 | 10 | 4 | US-09-535-852-1090 |
| 2 | 33 | 45.8 | 10 | 4 | US-09-535-852-1090 |
| 3 | 30 | 41.7 | 8 | 2 | US-08-520-535-12 |
| 4 | 30 | 41.7 | 8 | 2 | US-08-520-535-12 |
| 5 | 30 | 41.7 | 9 | 2 | US-08-079-432-12 |
| 6 | 30 | 41.7 | 9 | 4 | US-08-986-234-92 |
| 7 | 30 | 41.7 | 9 | 4 | US-09-311-784A-374 |
| 8 | 30 | 41.7 | 9 | 4 | US-09-790-497A-1 |
| 9 | 30 | 41.7 | 10 | 3 | US-09-108-709-22 |
| 10 | 29 | 40.3 | 5 | 1 | US-07-946-237-4 |
| 11 | 29 | 40.3 | 5 | 2 | US-08-530-566-10 |
| 12 | 29 | 40.3 | 5 | 3 | US-09-195-726-10 |
| 13 | 29 | 40.3 | 5 | 3 | US-09-067-755-10 |
| 14 | 29 | 40.3 | 5 | 4 | US-08-239-785C-4 |
| 15 | 29 | 40.3 | 7 | 4 | US-09-069-827A-94 |
| 16 | 29 | 40.3 | 9 | 4 | US-09-069-827A-94 |
| 17 | 29 | 40.3 | 10 | 2 | US-08-735-253-8 |
| 18 | 29 | 40.3 | 10 | 2 | US-08-735-253-13 |
| 19 | 29 | 40.3 | 10 | 3 | US-08-481-968A-21 |
| 20 | 29 | 40.3 | 10 | 3 | US-08-154-712B-21 |
| 21 | 29 | 40.3 | 10 | 4 | US-09-947-925A-21 |
| 22 | 28 | 38.9 | 8 | 3 | US-09-315-304B-1649 |
| 23 | 28 | 38.9 | 10 | 1 | US-08-250-789A-119 |
| 24 | 28 | 38.9 | 10 | 4 | US-09-462-917A-73 |
| 25 | 28 | 38.9 | 10 | 4 | US-09-125-641-3 |
| 26 | 28 | 38.9 | 10 | 4 | US-09-790-497A-5 |
| 27 | 28 | 38.9 | 10 | 4 | US-09-790-497A-24 |

28 27.5 38.2 6 1 US-08-191-571-12 Sequence 12, Appl
29 27.5 38.2 6 5 PCT-US95-00296-12 Sequence 12, Appl
30 27 37.5 8 3 US-08-925-002-12 Sequence 12, Appl
31 27 37.5 8 3 US-08-586-670A-17 Sequence 17, Appl
32 27 37.5 8 3 US-09-082-279B-1495 Sequence 1495, Ap
33 27 37.5 8 4 US-09-834-784-1495 Sequence 1495, Ap
34 27 37.5 8 4 US-09-910-552-12 Sequence 12, Appl
35 27 37.5 8 4 US-09-350-641C-1650 Sequence 1650, Ap
36 27 37.5 10 3 US-09-315-304B-1587 Sequence 1587, Ap
37 27 37.5 10 4 US-09-350-325-47 Sequence 47, Appl
38 27 37.5 10 4 US-09-535-852-1357 Sequence 1357, Ap
39 27 37.5 10 4 US-09-350-641C-1587 Sequence 1587, Ap
40 27 37.5 10 4 US-09-239-043D-2474 Sequence 2474, Ap
41 27 37.5 10 4 US-09-620-091-28 Sequence 28, Appl
42 27 37.5 10 4 US-09-620-091-42 Sequence 42, Appl
43 27 37.5 10 4 US-09-620-091-42 Sequence 42, Appl
44 26.5 36.8 10 3 US-09-186-958-12 Sequence 12, Appl
45 26.5 36.8 10 3 US-09-669-271A-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-535-852-1090
; Sequence 1090, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535.852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1090
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-09-535-852-1090

Query Match 45.8%; Score 33; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTTGWC 10
||| |
Db 1 CGYALDARGC 10

RESULT 2

US-09-535-852-1352
; Sequence 1352, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535.852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1352
; LENGTH: 10

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocoilin-1 cell adhesion recognition sequence
US-09-535-852-1352

Query Match          45.8%; Score 33; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
    ||| |||
Db 1 CGYATTADGC 10

RESULT 3
US-08-520-535-12
; Sequence 12, Application US/08520535
; Patent No. 5817750
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,535
; FILING DATE: 28-AUG-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-08-520-535-12

Query Match          41.7%; Score 30; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGYWL 5
    . |||
Db 1 CDYWL 5

RESULT 4
US-09-079-432-12
; Sequence 12, Application US/09079432
; Patent No. 5955572
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
```

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,432
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/520,535
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-09-079-432-12

Query Match          41.7%; Score 30; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGYWL 5
    . |||
Db 1 CDYWL 5

RESULT 5
US-08-986-234-92
; Sequence 92, Application US/08986234
; Patent No. 5981706
; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-08-986-234-92

Query Match          41.7%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
    . |||
Db 2 IWGC 5

RESULT 6
US-09-311-784A-374
; Sequence 374, Application US/09311784A
; Patent No. 6534482
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GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 ENV 69 (peptide 25.0113)
US-09-311-784A-374

Query Match 41.7%; Score 30; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
DB 1 IWGC 4
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RESULT 7
US-09-790-497A-1
; Sequence 1, Application US/09790497A
; Patent No. 6649735
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-16
; CURRENT APPLICATION NUMBER: US/09/790,497A
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/576,824
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-790-497A-1

Query Match 41.7%; Score 30; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
DB 1 IWGC 4
|||||

Db 1 IWGC 4

RESULT 8
US-09-108-709-22
; Sequence 22, Application US/09108709
; Patent No. 6008044
; GENERAL INFORMATION:
; APPLICANT: Cottropia, Joseph P.
; TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane G1
; FILE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis T
; TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibiting
; TITLE OF INVENTION: Fusion-associated Epitope (GCSGKLIC) in gp-41
; FILE REFERENCE: 10586/00406
; CURRENT APPLICATION NUMBER: US/09/108,709
; CURRENT FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: amino acids 600-609 according to the Gnan
; OTHER INFORMATION: numbering system
US-09-108-709-22

Query Match 41.7%; Score 30; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
DB 1 IWGC 4
|||||

RESULT 9
US-09-790-497A-110
; Sequence 110, Application US/09790497A
; Patent No. 6649735
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-16
; CURRENT APPLICATION NUMBER: US/09/790,497A
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/576,824
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-790-497A-110

Query Match 41.7%; Score 30; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
|
|
|
|
Db 1 IWGC 4

RESULT 10

US-07-946-237-4
; Sequence 4, Application US/07946237
; Patent No. 5348874
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,237
FILING DATE: 19920914

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: David E. Brook
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BT92-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
MOLECULE TYPE: peptide
US-07-946-237-4

Query Match 40.3%; Score 29; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
|
|
|
|
Db 2 VWGC 5

RESULT 11

US-08-530-566-10
; Sequence 10, Application US/08530566
; Patent No. 5840865
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,566
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,765
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.

REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BT92-01ZA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-530-566-10

Query Match 40.3%; Score 29; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
|
|
|
|
Db 2 VWGC 5

RESULT 12

US-09-195-726-10
; Sequence 10, Application US/09195726
; Patent No. 6159717
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02421

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,726
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/530,566
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,765
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: IMB92-012AZ
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-195-726-10

Query Match 40.3%; Score 29; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

Qy 7 IWGC 10
Db 2 VWGC 5

RESULT 13
US-09-067-755-10
Sequence 10, Application US/09067755
Patent No. 6225121
GENERAL INFORMATION:
APPLICANT: Savakis, Charalambos
APPLICANT: Franz, Gerald H.
APPLICANT: Loukeris, Athanasios
APPLICANT: Klinakis, Apostolos G.
TITLE OF INVENTION: Eukaryotic transposable Element
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,755
FILING DATE: 27-APR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/530,566
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,765
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: IMB92-012AZ
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-067-755-10

Query Match 40.3%; Score 29; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

Qy 7 IWGC 10
Db 2 VWGC 5

RESULT 14
US-08-239-765C-4
Sequence 4, Application US/08239765C
Patent No. 6469228
GENERAL INFORMATION:
APPLICANT: Savakis, Charalambos
APPLICANT: Franz, Gerald H.
APPLICANT: Loukeris, Athanasios
TITLE OF INVENTION: Eukaryotic transposable Element
FILE REFERENCE: 18747/1130
CURRENT APPLICATION NUMBER: US/08/239,765C
CURRENT FILING DATE: 1994-05-09
PRIOR APPLICATION NUMBER: 07/946,237
PRIOR FILING DATE: 1992-09-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 5
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Conserved amino acid sequence of the TC-1 family of transposable elements
OTHER INFORMATION: elements
US-08-239-765C-4

Query Match 40.3%; Score 29; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

Qy 7 IWGC 10
Db 2 VWGC 5

RESULT 15
US-09-069-827A-94
Sequence 94, Application US/09069827A
Patent No. 6617114
GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M
KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DERUYSCHE, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,827A
; FILING DATE: 30-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/050,359
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: PCT/US97/19638
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: US 08/740,671
; FILING DATE: 31-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOWLKES=4C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:
;
US-09-069-827A-94

Query Match 40.3%; Score 29; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YWLTING 9
Db 1 YWPPDWG 7

Search completed: December 30, 2004, 14:44:16
Job time : 24.6667 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 14:43:15 ; Search time 81.3333 Seconds
(without alignments)
44.229 Million cell updates/sec

Title: US-10-046-922-35

Perfect score: 72

Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 182644

Minimum DB seq length: 0

Maximum_DB_seq_length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:**
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 72 | 100.0 | 10 | 13 | US-10-046-922-35 |
| 2 | 54 | 75.0 | 10 | 13 | US-10-046-922-34 |
| 3 | 50 | 69.4 | 10 | 13 | US-10-046-922-73 |
| 4 | 33 | 45.8 | 7 | 13 | US-10-046-922-67 |
| 5 | 33 | 45.8 | 8 | 13 | US-10-046-922-68 |
| 6 | 33 | 45.8 | 10 | 17 | US-10-654-578-1090 |
| 7 | 33 | 45.8 | 10 | 17 | US-10-654-578-1352 |
| 8 | 32 | 44.4 | 10 | 8 | US-08-821-739A-90 |
| 9 | 32 | 44.4 | 10 | 14 | US-10-133-210-39 |
| 10 | 32 | 44.4 | 10 | 14 | US-10-133-210-69 |
| 11 | 31 | 43.1 | 9 | 13 | US-10-046-922-56 |
| 12 | 31 | 43.1 | 10 | 10 | US-09-572-404B-1454 |
| 13 | 30 | 41.7 | 9 | 8 | US-08-821-739A-78 |

14 30 41.7 9 9 US-09-832-723-104 Sequence 104, App
15 30 41.7 9 9 US-09-894-018-80 Sequence 80, Appl
16 30 41.7 9 9 US-09-894-018-185 Sequence 185, App
17 30 41.7 9 14 US-10-303-331-104 Sequence 104, App
18 30 41.7 9 14 US-10-371-525-374 Sequence 374, App
19 30 41.7 9 14 US-10-371-525-374 Sequence 374, App
20 30 41.7 9 14 US-10-371-645-374 Sequence 374, App
21 30 41.7 9 14 US-10-371-645-374 Sequence 374, App
22 30 41.7 9 17 US-10-474-960A-80 Sequence 80, Appl
23 30 41.7 9 17 US-10-474-960A-185 Sequence 185, App
24 30 41.7 10 15 US-10-462-452-707 Sequence 707, App
25 30 41.7 10 15 US-10-601-953-812 Sequence 812, App
26 30 41.7 10 16 US-10-322-266-708 Sequence 708, App
27 29 40.3 5 8 US-08-239-765B-4 Sequence 4, Appl
28 29 40.3 9 9 US-09-894-018-154 Sequence 154, App
29 29 40.3 9 14 US-10-133-210-8 Sequence 8, Appl
30 29 40.3 9 14 US-10-371-525-348 Sequence 348, App
31 29 40.3 9 14 US-10-371-525-348 Sequence 348, App
32 29 40.3 9 14 US-10-371-645-348 Sequence 348, App
33 29 40.3 9 14 US-10-371-645-348 Sequence 348, App
34 29 40.3 9 15 US-10-182-252A-180 Sequence 180, App
35 29 40.3 9 15 US-10-182-252A-181 Sequence 181, App
36 29 40.3 9 15 US-10-182-252A-305 Sequence 305, App
37 29 40.3 9 15 US-10-182-252A-792 Sequence 792, App
38 29 40.3 9 15 US-10-182-252A-793 Sequence 793, App
39 29 40.3 9 15 US-10-182-252A-837 Sequence 837, App
40 29 40.3 9 15 US-10-182-252A-838 Sequence 838, App
41 29 40.3 9 15 US-10-182-252A-1271 Sequence 1271, App
42 29 40.3 9 17 US-10-474-960A-154 Sequence 154, App
43 29 40.3 10 8 US-08-821-739A-92 Sequence 92, Appl
44 29 40.3 10 9 US-09-947-925A-21 Sequence 21, Appl
45 29 40.3 10 14 US-10-094-401-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046.922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match 100.0%; Score 72; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGYWLTIWGC 10
|||||
Db 1 CGYWLTIWGC 10

RESULT 2
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki

; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046.922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match 75.0%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9
Db 2 GYWLTIWG 9

RESULT 3
US-10-046-922-73
; Sequence 73, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046.922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 10
; TYPE: PRT
; ORGANISM: peptide library
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(7)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (9)..(9)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-73

Query Match 69.4%; Score 50; DB 13; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
Db 1 CGYWXXXWC 10

RESULT 4
US-10-046-922-67
; Sequence 67, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime

; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046.922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X at position 4-6 is any amino acid
US-10-046-922-67

Query Match 45.8%; Score 33; DB 13; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
Db 1 GYWXXXW 7

RESULT 5
US-10-046-922-68
; Sequence 68, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046.922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 8
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (8)..(8)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-68

Query Match 45.8%; Score 33; DB 13; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
Db 1 GYWXXXW 7

RESULT 6
US-10-654-578-1090
; Sequence 1090, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654.578

```
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1090
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-10-654-578-1090

Query Match      45.8%; Score 33; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYMLTWGC 10
Db 1 CGYALDARGC 10

RESULT 7
US-10-654-578-1352
; Sequence 1352, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1352
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-10-654-578-1352

Query Match      45.8%; Score 33; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYMLTWGC 10
Db 1 CGYATTADGC 10

RESULT 8
US-08-821-739A-90
; Sequence 90, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
```

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; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-90

Query Match      44.4%; Score 32; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LTIWGC 10
Db 2 LGIWGC 7

RESULT 9
US-10-133-210-39
; Sequence 39, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-03SAX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-39

Query Match      44.4%; Score 32; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LTIWGC 10
Db 2 LGIWGC 7

RESULT 10
US-10-133-210-69
; Sequence 69, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
```

; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-69

Query Match 44.4%; Score 32; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LTIWGC 10
| | | | |
Db 2 LGIWGC 7

RESULT 11
US-10-046-922-36
; Sequence 36, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-36

Query Match 43.1%; Score 31; DB 13; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
| | | | |
Db 2 GYWDTW 8

RESULT 12
US-09-572-404B-1454
; Sequence 1454, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1454
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in p2RY5 at 139-148 and may interact with Sequen

; OTHER INFORMATION: in this patent.
US-09-572-404B-1454

Query Match 43.1%; Score 31; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYWLTIW 9
| | | | |
Db 1 GYWLTVIG 8

RESULT 13
US-08-821-739A-78
; Sequence 78, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-78

Query Match 41.7%; Score 30; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
| | | | |
Db 1 IWGC 4

RESULT 14
US-09-832-723-104
; Sequence 104, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11

```

; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-104

```

```

Query Match      41.7%; Score 30; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIW 8
Db 1 CTLMPTFW 8

```

```

RESULT 15
US-09-894-018-80
; Sequence 80, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-09-894-018-80

```

```

Query Match      41.7%; Score 30; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
Db 1 IWGC 4

```

Search completed: December 30, 2004, 15:04:06
Job time : 81.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2004, 14:30:43 ; Search time 18.6667 Seconds
(without alignments)
51.545 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 24 | 33.3 | 10 | 2 S71868 | glutathione trans |
| 2 | 24 | 33.3 | 10 | 2 A35556 | hypothetical prote |
| 3 | 22 | 30.6 | 7 | 2 P70586 | T-cell receptor be |
| 4 | 22 | 30.6 | 10 | 2 T17075 | cytochrome-c oxida |
| 5 | 21 | 29.2 | 10 | 2 E41946 | T-cell receptor ga |
| 6 | 20 | 27.8 | 5 | 2 JH0253 | gut pentapeptide - |
| 7 | 20 | 27.8 | 6 | 2 F41946 | T-cell receptor ga |
| 8 | 20 | 27.8 | 8 | 2 S19288 | acylase - Kluysera |
| 9 | 19 | 26.4 | 9 | 2 P70324 | Ig heavy chain CRD |
| 10 | 19 | 26.4 | 10 | 2 P70289 | Ig heavy chain CRD |
| 11 | 19 | 26.4 | 10 | 2 E49033 | T-cell receptor ga |
| 12 | 19 | 26.4 | 10 | 2 F49033 | T-cell receptor ga |
| 13 | 19 | 26.4 | 10 | 2 C41946 | T-cell receptor ga |
| 14 | 18 | 25.0 | 8 | 2 J80315 | leucokinin V - Mad |
| 15 | 18 | 25.0 | 10 | 2 P70230 | Ig heavy chain CRD |
| 16 | 18 | 25.0 | 10 | 2 P70923 | T-cell receptor be |
| 17 | 18 | 25.0 | 10 | 2 F33932 | Ig mu chain J regi |
| 18 | 18 | 25.0 | 10 | 4 S14943 | UGA3 leader peptid |
| 19 | 17 | 23.6 | 4 | 2 B53284 | T-cell receptor be |
| 20 | 17 | 23.6 | 6 | 2 P70629 | T-cell receptor be |
| 21 | 17 | 23.6 | 6 | 2 P70637 | T-cell receptor be |
| 22 | 17 | 23.6 | 6 | 2 A61068 | locustakinin - mlg |
| 23 | 17 | 23.6 | 6 | 4 I79564 | hypothetical TGL3 |
| 24 | 17 | 23.6 | 7 | 2 P70628 | T-cell receptor be |
| 25 | 17 | 23.6 | 7 | 2 P70642 | T-cell receptor be |
| 26 | 17 | 23.6 | 7 | 2 P70722 | T-cell receptor be |
| 27 | 17 | 23.6 | 7 | 2 P70728 | T-cell receptor be |
| 28 | 17 | 23.6 | 7 | 2 PX0008 | glucuronosyltransf |
| 29 | 17 | 23.6 | 7 | 2 B48394 | major fat-globule |

| | | | | | |
|----|----|------|----|----------|--------------------|
| 30 | 17 | 23.6 | 7 | 2 PD0029 | pev-kinin 1 - pena |
| 31 | 17 | 23.6 | 7 | 2 S57274 | triacylglycerol li |
| 32 | 17 | 23.6 | 7 | 2 S33244 | neuromodulatory pe |
| 33 | 17 | 23.6 | 7 | 2 S33245 | neuromodulatory pe |
| 34 | 17 | 23.6 | 7 | 2 S33246 | neuromodulatory pe |
| 35 | 17 | 23.6 | 8 | 2 P70724 | T-cell receptor be |
| 36 | 17 | 23.6 | 8 | 2 J80316 | leucokinin VI - Ma |
| 37 | 17 | 23.6 | 8 | 2 J80317 | leucokinin VII - M |
| 38 | 17 | 23.6 | 8 | 2 J80318 | leucokinin VIII - |
| 39 | 17 | 23.6 | 8 | 2 A31570 | angiotensin-conver |
| 40 | 17 | 23.6 | 9 | 2 A24244 | adipokinetic hormo |
| 41 | 17 | 23.6 | 9 | 2 P70634 | T-cell receptor be |
| 42 | 17 | 23.6 | 9 | 2 P70562 | T-cell receptor be |
| 43 | 17 | 23.6 | 9 | 2 A60522 | sperm-activating p |
| 44 | 17 | 23.6 | 10 | 2 B33995 | hypotrehalosemic h |
| 45 | 17 | 23.6 | 10 | 2 S08997 | hypertrehalosemic |

ALIGNMENTS

RESULT 1

S71868

glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment)

N:Alternate names: glutathione S-transferase class mu 4

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: S71868

R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.

Biochem. J. 317, 879-884, 1996

A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospra

A:Reference number: S71864; MUID:96332484; PMID:8760377

A:Accession: S71868

A:Molecule type: Protein

A:Residues: 1-10 <R0U>

A:Cross-references: UNIPROT:Q7M3E8

C:Comment: At least five species-independent classes of cytosolic glutathion transferase

s mitochondrial form are known.

C:Complex: dimer

C:Function:

A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a

A:Pathway: detoxification; xenobiotics metabolism

A>Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism

es of damage

C:Superfamily: glutathione transferase

C:Keywords: dimer; transferase

Query Match 33.3%; Score 24; DB 2; Length 10;

Best Local Similarity 100.0%; Pred.No. 9.9e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4

DB 4 GYW 6

RESULT 2

A35556

hypothetical protein (ODC region) - human

C:Species: Homo sapiens (man)

C>Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993

C:Accession: A35556

R:Moahier, J.A.; Gilbert, J.D.; Skunca, M.; Doseescu, J.; Almodovar, K.M.; Luk, G.D.

J. Biol. Chem. 265, 4884-4892, 1990

A:Title: Isolation and expression of a human ornithine decarboxylase gene.

A:Reference number: A35556; MUID:90202959; PMID:2318872

A:Accession: A35556

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-10 <MOS>

A:Cross-references: GB:J05271

Query Match

33.3%; Score 24; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGYW 4
Db 5 CGAW 8

RESULT 3
PT0586
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0586; PT0592
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Functional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0586
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <PEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor

Query Match 30.6%; Score 22; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TIWG 9
Db 3 SIWG 6

RESULT 4
T17075
cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)
C;Species: mitochondrion Chamaeleo fischeri
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17075
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene
A;Reference number: Z18674; MUID:97315309; PMID:9169559
A;Accession: T17075
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: UNIPROT:O79912; EMBL:U82688; NID:g3603112; PID:g3603115; PIDN:AAC622
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 30.6%; Score 22; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLTIW 8
Db 2 WLLRW 6

RESULT 5
E41946
T-cell receptor gamma chain (1a.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: E41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: E41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <WHE>
C;Keywords: T-cell receptor

Query Match 29.2%; Score 21; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWL 5
Db 2 CAVWI 6

RESULT 6
JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric
, and of the circular muscle of the gastro-intestinal junction.

Query Match 27.8%; Score 20; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYW 4
Db 1 GFW 3

RESULT 7
F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: F41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <WHE>
C;Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWL 5
Db 2 CAVWV 6

RESULT 8
S19288
acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 659-662, 1991

A:Title: Chemical modification of serine at the active site of penicillin acylase from *Streptomyces clavuligerus*

A:Reference number: S19288; MUID:92105664; PMID:1764029

A:Accession: S19288

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAR>

A:Cross-references: UNIPROT:C7M124

Query Match 27.8%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
PT0324
IG heavy chain CRD3 region (clone J2-106C) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0324
C/Ramada, M.; Wesserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0324
A/Molecule type: DNA
A/Residues: 1-9 <I>AM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

```
Query Match      26.4%; Score 19; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. NO. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```

RESULT 10
PT0289
IG heavy chain CRD3 region (clone 4-109) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0289
R;Yamada, M.; Wesserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0289
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

```

```
Query Match      26.4%; Score 19; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 5.4e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

RESULT 11
E49033
T-cell receptor gamma chain V-D-J region - human (fragment).
C;Species: Homo sapiens (man)
C;date: 19-Dec-1993 #sequence revision 25-Aug-1995 #text change 21-Jul-2000

C;Accession: E49033; D49033
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2989-3007, 1991
A>Title: Functionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID: 92083926; PMID:1684157

| | | | | |
|-----------------------|--------|--------------------|-------|---------------|
| Query Match | 26.4% | Score 19; | DB 2; | Length 10; |
| Best Local Similarity | 50.0%; | Pred. No. 5.4e+03; | | |
| Matches | 2; | Conservative | 0; | Mismatches 2; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

RESULT 12
F49033
T-cell receptor gamma chain V-D-J region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: F49033
R:Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
A>Title: Functionally distinct subsets of human gamma/delta T cells.
A:Reference number: A49033; MUID:92083926; PMID:1684157

| | | | | |
|-------------------------|--------|--------------------|-----------|------------|
| Query Match | 26.4% | Score 19; | DB 2; | Length 10; |
| Best Local Similarity | 50.0%; | Fred. No. 5.4e+03; | | |
| Matches 2; Conservative | 0; | Mismatches 2; | Indels 0; | Gaps 0; |

RESULT 13
C41946
T-cell receptor gamma chain (1t.60) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: C41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: C41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <WHE>
C:Keywords: T-cell receptor

| | | | | |
|-----------------------|-------|-----------|----------|------------|
| Query Match | 26.4% | Score 19; | DB 2; | Length 10; |
| Best Local Similarity | 50.0% | Pred. No. | 5.4e+03; | |

Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYW 4
|
Db 2 CAVW 5

RESULT 14

JS0315

Leucokinin V - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0315
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
A;Reference number: JS0315
A;Accession: JS0315
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19987
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
P;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 25.0%; Score 18; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9
|
Db 1 GSGFSSWG 8

RESULT 15

PT0230

Ig heavy chain CDR3 region (clone 1-118A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0230
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0230
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 18; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9
|
Db 3 ITIEG 7

Search completed: December 30, 2004, 14:45:18
Job time : 19.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 14:22:33 ; Search time 100 Seconds
(without alignments)
57.537 Million cell updates/sec

Title: US-10-046-922-35

Perfect score: 72

Sequence: 1 GYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|----------------------|
| 1 | 30.5 | 42.4 | 10 | 1 LABA_JATMU | P13270 jatropha mu |
| 2 | 27 | 37.5 | 10 | 2 Q8SHF6 | Q8shf6 chamaeleo m |
| 3 | 26 | 36.1 | 8 | 2 Q70Y57 | Q70y57 fuerstia af |
| 4 | 26 | 36.1 | 8 | 2 CAD45547 | Cad45547 fuerstia af |
| 5 | 24 | 33.3 | 10 | 2 Q7M3E8 | Q7m3e8 sus scrofa |
| 6 | 24 | 33.3 | 10 | 2 Q8SHN1 | Q8shn1 bradypodion |
| 7 | 24 | 33.3 | 10 | 2 Q6JL97 | Q6jl97 neisseria g |
| 8 | 24 | 33.3 | 10 | 2 AAS16521 | Aas16521 neisseria g |
| 9 | 23.5 | 32.6 | 9 | 2 Q85DB0 | Q85db0 lepitemur s |
| 10 | 23.5 | 32.6 | 9 | 2 Q85DB8 | Q85db8 lepitemur e |
| 11 | 23.5 | 32.6 | 9 | 2 Q94NA9 | Q94na9 daubentonia |
| 12 | 23.5 | 32.6 | 9 | 2 Q94NB0 | Q94nb0 microcebus |
| 13 | 23.5 | 32.6 | 9 | 2 Q94NB1 | Q94nb1 microcebus |
| 14 | 23.5 | 32.6 | 9 | 2 Q94NB2 | Q94nb2 microcebus |
| 15 | 23.5 | 32.6 | 9 | 2 Q94XE6 | Q94xe6 tectocoris |
| 16 | 23 | 31.9 | 10 | 2 Q8SHC6 | Q8shc6 furcifer be |
| 17 | 22 | 30.6 | 10 | 2 Q79912 | Q79912 chamaeleo f |
| 18 | 22 | 30.6 | 10 | 2 Q9G697 | Q9g697 chamaeleo d |
| 19 | 22 | 30.6 | 10 | 2 Q8SH83 | Q8sh83 brookesia t |
| 20 | 22 | 30.6 | 10 | 2 Q8SH85 | Q8sh85 brookesia t |
| 21 | 22 | 30.6 | 10 | 2 Q8SH88 | Q8sh88 brookesia t |
| 22 | 22 | 30.6 | 10 | 2 Q8SH90 | Q8sh90 brookesia s |
| 23 | 22 | 30.6 | 10 | 2 Q8SH96 | Q8sh96 brookesia s |
| 24 | 22 | 30.6 | 10 | 2 Q8SHA2 | Q8sha2 brookesia p |
| 25 | 22 | 30.6 | 10 | 2 Q8SHA5 | Q8sha5 brookesia a |
| 26 | 22 | 30.6 | 10 | 2 Q8SHC9 | Q8shc9 furcifer ba |
| 27 | 22 | 30.6 | 10 | 2 Q8SHD2 | Q8shd2 chamaeleo w |
| 28 | 22 | 30.6 | 10 | 2 Q8SHD5 | Q8shd5 chamaeleo s |
| 29 | 22 | 30.6 | 10 | 2 Q8SHD8 | Q8shd8 chamaeleo r |
| 30 | 22 | 30.6 | 10 | 2 Q8SHE1 | Q8she1 chamaeleo q |
| 31 | 22 | 30.6 | 10 | 2 Q8SHE4 | Q8she4 chamaeleo q |

| | | | | | |
|----|----|------|----|----------|--------------------|
| 32 | 22 | 30.6 | 10 | 2 Q8SHE7 | Q8she7 chamaeleo p |
| 33 | 22 | 30.6 | 10 | 2 Q8SHF3 | Q8shf3 chamaeleo m |
| 34 | 22 | 30.6 | 10 | 2 Q8SHF9 | Q8shf9 chamaeleo j |
| 35 | 22 | 30.6 | 10 | 2 Q8SHG5 | Q8shg5 chamaeleo h |
| 36 | 22 | 30.6 | 10 | 2 Q8SHG8 | Q8shg8 chamaeleo g |
| 37 | 22 | 30.6 | 10 | 2 Q8SHH1 | Q8shh1 chamaeleo f |
| 38 | 22 | 30.6 | 10 | 2 Q8SHH4 | Q8shh4 chamaeleo f |
| 39 | 22 | 30.6 | 10 | 2 Q8SHH7 | Q8shh7 chamaeleo e |
| 40 | 22 | 30.6 | 10 | 2 Q8SHI0 | Q8shi0 chamaeleo d |
| 41 | 22 | 30.6 | 10 | 2 Q8SHI3 | Q8shi3 chamaeleo c |
| 42 | 22 | 30.6 | 10 | 2 Q8SHI6 | Q8shi6 chamaeleo c |
| 43 | 22 | 30.6 | 10 | 2 Q8SHI9 | Q8shi9 chamaeleo c |
| 44 | 22 | 30.6 | 10 | 2 Q8SHJ2 | Q8shj2 chamaeleo a |
| 45 | 22 | 30.6 | 10 | 2 Q8SHJ5 | Q8shj5 calumma par |

ALIGNMENTS

RESULT 1

LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Labaditin.
OS Jatropha multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaceae;
OC Jatropha.
OX NCBI_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=Latex;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
multifida L. (Euphorbiaceae). Isolation and sequence determination by
RT means of two-dimensional NMR";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the
CC classical pathway of complement activation in vitro. Activity
CC seems to be based on an interaction with C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine
CC for treatment of infected wounds, skins infections and scabies.
KW Direct protein sequencing.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 42.4%; Score 30.5; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 2 GYWLTIWGC 9
| | | | |
Db 2 GVV-TVWG 8

RESULT 2

Q8SHF6
ID Q8SHF6 PRELIMINARY; PRT; 10 AA.
AC Q8SHF6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Chamaeleo melleri (Meller's chameleon).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OX NCBI_TaxID=179915;

| | | |
|-----------|--|--|
| DT | 20-MAY-2004 | (TEMBLrel. 27, Created) |
| DT | 20-MAY-2004 | (TEMBLrel. 27, Last sequence update) |
| DT | 20-MAY-2004 | (TEMBLrel. 27, Last annotation update) |
| DN | NUOL | (Fragment). |
| GN | Neisseria gonorrhoeae. | |
| OS | Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; | |
| OC | Neisseriaceae; Neisseria. | |
| OX | NCBI_TaxID=485; | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RC | STRAIN=MS11; | |
| RA | Snyder L.A., Davies J.K., Saunders N.J.; | |
| RT | "Microarray genotyping of key experimental strains of Neisseria | |
| RT | gonorrhoeae reveals gene complement diversity and five new neisserial | |
| RT | genes associated with Minimal Mobile Elements."; | |
| RL | BMC Genomics 5:23-23(2004). | |
| RN | [2] | |
| RP | SEQUENCE FROM N.A. | |
| RC | STRAIN=MS11; | |
| RA | Snyder L.A.S., Davies J.K., Saunders N.J.; | |
| RL | Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases. | |
| DR | EMBL; AY386266; AAS16521.1; - | |
| FT | NON TER 1 | |
| SQ | SEQUENCE 10 AA; 1227 MW; BACCB286379D1A6 CRC64; | |
| | Query Match 33.3%; Score 24; DB 2; Length 10; | |
| | Best Local Similarity 60.0%; Pred. No. 4.8e+03; | |
| | Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0; | |
| QY | 5 LTIWG 9 | |
| | : | |
| Db | 3 MTFWG 7 | |
| | : | |
| RESULT 9 | | |
| Q85DB0 | PRELIMINARY; PRT; 9 AA. | |
| ID | Q85DB0 | |
| AC | Q85DB0; | |
| DT | 01-JUN-2003 (TEMBLrel. 24, Created) | |
| DT | 01-JUN-2003 (TEMBLrel. 24, Last sequence update) | |
| DT | 01-OCT-2003 (TEMBLrel. 25, Last annotation update) | |
| DE | Cytochrome oxidase subunit III (Fragment). | |
| DE | Names-COIII; | |
| OS | Lepilemur septentrionalis (northern sportive lemur). | |
| OG | Mitochondrion. | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC | Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur. | |
| OX | NCBI_TaxID=78584; | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RC | MEDLINE=22631663; PubMed=12719521; | |
| RA | Pastorini J., Thalmann U., Martin R.D.; | |
| RT | "A molecular approach to comparative phylogeography of extant Malagasy | |
| RT | lemurs."; | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003). | |
| DR | EMBL; AF224597; AAP33652.1; - | |
| GO | GO: 0005739; C:mitochondrion; IEA. | |
| KW | Mitochondrion. | |
| FT | NON TER 1 | |
| SQ | SEQUENCE 9 AA; 1174 MW; 16C563636B5045B0 CRC64; | |
| | Query Match 32.6%; Score 23.5; DB 2; Length 9; | |
| | Best Local Similarity 57.1%; Pred. No. 1.8e+06; | |
| | Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1; | |
| QY | 3 YWLTIWG 9 | |
| | : | |
| Db | 5 YW---WG 8 | |
| | : | |
| RESULT 10 | | |

Q85DB8
ID Q85DB8 PRELIMINARY; PRT; 9 AA.
AC Q85DB8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Lepilemur edwardsi (Milne-Edwards's sportive lemur).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
OX NCBI_TaxID=122230;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224595; AAK3644.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;
Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 3 YWLTWIG 9
DB 5 YW---WG 8

RESULT 11
Q94NA9
ID Q94NA9 PRELIMINARY; PRT; 9 AA.
AC Q94NA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Daubentonia madagascariensis (Aye-aye).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Daubentonidae;
OC Daubentonia.
OX NCBI_TaxID=31869;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family Cheirogaleidae (Primates) based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22281620; PubMed=12393004;
RA Pastorini J., Forstner M.R., Martin R.D.;
RT "Phylogenetic relationships among Lemuridae (Primates): evidence from mtDNA.";
RL J. Hum. Evol. 43:463-478(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224641; AAK70615.1; -.
DR EMBL; AF224642; AAK70619.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;
Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 3 YWLTWIG 9
DB 5 YW---WG 8

RESULT 12
Q94NB0
ID Q94NB0 PRELIMINARY; PRT; 9 AA.
AC Q94NB0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Microcebus rufus (Brown mouse lemur).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=122232;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family Cheirogaleidae (Primates) based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224636; AAK70595.1; -.
DR EMBL; AF224637; AAK70599.1; -.
DR EMBL; AF224638; AAK70603.1; -.
DR EMBL; AF224639; AAK70607.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;
Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 3 YWLTWIG 9
DB 5 YW---WG 8

RESULT 13
Q94NB1
ID Q94NB1 PRELIMINARY; PRT; 9 AA.
AC Q94NB1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Microcebus ravelobensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OX Microcebus.
RN [1]
RP NCBI_TaxID=122231;
RX SEQUENCE FROM N.A.
RA MEDLINE=21184272; PubMed=11286490;
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences."
RL Mol. Phylogenet. Evol. 19:45-56(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs."
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224630; AAK70571.1; -;
DR EMBL; AF224631; AAK70575.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTWIG 9
DB 5 YW---WG 8

RESULT 14
Q94NB2
ID Q94NB2 PRELIMINARY; PRT; 9 AA.
AC Q94NB2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Microcebus murinus (Lesser mouse lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=30608;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences."
RL Mol. Phylogenet. Evol. 19:45-56(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs."
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224624; AAK70547.1; -;
DR EMBL; AF224625; AAK70551.1; -;
DR EMBL; AF224626; AAK70555.1; -;
DR EMBL; AF224627; AAK70559.1; -;
DR EMBL; AF224628; AAK70563.1; -;
DR EMBL; AF224629; AAK70567.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTWIG 9
DB 5 YW---WG 8

RESULT 15
Q94XE6
ID Q94XE6 PRELIMINARY; PRT; 9 AA.
AC Q94XE6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit III (Fragment).
GN Name=cox3;
OS Tectocoris diophthalmus (cotton harlequin bug).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Paraheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC Tectocoris.
OX NCBI_TaxID=159956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396409; PubMed=11504862;
RA Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;
RT "Increased rate of gene rearrangement in the mitochondrial genomes of
three orders of hemipteroid insects."
RL Mol. Biol. Evol. 18:1828-1832(2001).
DR EMBL; AF335990; AAK55283.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTWIG 9
DB 5 YW---WG 8

Search completed: December 30, 2004, 14:43:05
Job time : 100 secs

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| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|----------|--------------------|
| | Score | Match | Length | | | |
| 1 | 54 | 100.0 | 10 | 5 | ABP53931 | Abp53931 VEGFR-3 b |
| 2 | 54 | 100.0 | 10 | 5 | ABP53932 | Abp53932 VEGFR-3 b |
| 3 | 43 | 79.6 | 13 | 6 | Aao26093 | Aao26093 Fc region |
| 4 | 43 | 79.6 | 13 | 8 | ADJ50760 | Adj50760 Human ser |
| 5 | 43 | 79.6 | 474 | 6 | ABU30004 | Abu30004 Protein e |
| 6 | 43 | 79.6 | 492 | 7 | ADC97318 | Adc97318 E. faeciu |
| 7 | 42 | 77.8 | 120 | 4 | AAb62247 | Aab62247 Human HIV |
| 8 | 42 | 77.8 | 1140 | 4 | AAS09365 | Aae09365 Human ATP |
| 9 | 42 | 77.8 | 1498 | 4 | AAS09362 | Aae09362 Mouse ATP |
| 10 | 42 | 77.8 | 1503 | 2 | AAV43544 | Aav43544 A Human M |
| 11 | 42 | 77.8 | 1503 | 4 | AAS09361 | Aae09361 Human ATP |
| 12 | 42 | 77.8 | 1503 | 4 | AAS09370 | Aae09370 Human ATP |
| 13 | 42 | 77.8 | 1503 | 4 | AAS09367 | Aae09367 Human ATP |
| 14 | 42 | 77.8 | 1503 | 4 | AAS09368 | Aae09368 Human ATP |
| 15 | 42 | 77.8 | 1503 | 4 | AAS09369 | Aae09369 Human ATP |
| 16 | 42 | 77.8 | 1503 | 4 | AAS09364 | Aae09364 Human ATP |
| 17 | 42 | 77.8 | 1503 | 4 | AAS09371 | Aae09371 Human ATP |
| 18 | 42 | 77.8 | 1503 | 4 | AAS09363 | Aae09363 Human ATP |
| 19 | 42 | 77.8 | 1503 | 5 | ABP52113 | Abp52113 Homo sapi |
| 20 | 41 | 75.9 | 14 | 6 | Aao26134 | Aao26134 Fc region |
| 21 | 41 | 75.9 | 14 | 8 | ADJ50801 | Adj50801 Human ser |
| 22 | 41 | 75.9 | 34 | 4 | ABB38460 | Abb38460 Peptide # |
| 23 | 41 | 75.9 | 34 | 4 | AAM31901 | Aam31901 Peptide # |
| 24 | 41 | 75.9 | 34 | 4 | AAM71604 | Aam71604 Human bra |
| 25 | 41 | 75.9 | 34 | 4 | AAM59071 | Aam59071 Human bra |

CC The present invention describes an isolated peptide (I) that binds to and

CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
 CC antidiabetic and vulnerary activities, and can be used in gene therapy.
 CC Compositions and methods from the present invention are useful for
 CC diagnosing, evaluating and treating disorders mediated by the activity of
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence
 CC represents a specifically claimed VEGFR-3 binding peptide from the
 CC present invention
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 54; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWLTIWG 8
 DB 2 GYWLTIWG 9
 RESULT 2
 ID ABP53932 standard; peptide; 10 AA.
 XX
 AC ABP53932;
 XX
 DT 09-JAN-2003 (first entry)
 XX
 DE VEGFR-3 binding peptide SEQ ID NO:35.
 XX
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
 KW vulnerary; cell surface receptor; cancer; neovascularisation;
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
 KW diabetes; PDGF; platelet derived growth factor.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200257299-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 16-JAN-2002; 2002WO-1B000099.
 XX
 PR 17-JAN-2001; 2001US-0262476P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 XX
 PI Alitalo K, Koivunen E, Kubo H;
 DR WPI; 2002-691521/74.
 XX
 PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
 PT such as cancer and diseases of neovascularization.
 XX
 PS Claim 13; Page 80; 149pp; English.
 CC
 CC The present invention describes an isolated peptide (I) that binds to and
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
 CC antidiabetic and vulnerary activities, and can be used in gene therapy.
 CC Compositions and methods from the present invention are useful for
 CC diagnosing, evaluating and treating disorders mediated by the activity of
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence
 CC represents a specifically claimed VEGFR-3 binding peptide from the
 CC present invention
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 54; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWLTIWG 8
 DB 2 GYWLTIWG 9
 RESULT 3
 ID AAO26093 standard; peptide; 13 AA.
 XX
 AC AAO26093;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Fc region binding peptide SEQ ID No 73.
 XX
 KW Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;
 KW antibody response; half-life; stability; circulatory system.
 XX
 OS Unidentified.
 XX
 PN WO200286070-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012492.
 XX
 PR 18-APR-2001; 2001US-0284534P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Rondon IJ, Wu Q, Ley AC, Stochl M, Ransohoff TC, Potter MD;
 XX
 DR WPI; 2003-201220/19.
 XX
 PT New polypeptides, useful as binding molecules for detecting, isolating or
 PT purifying immunoglobulin Fc-region polypeptides present in a solution, or
 PT for regulating or preventing an antibody response.
 XX
 PS Claim 3; Page 76; 152pp; English.
 CC
 CC The invention relates to novel isolated polypeptides comprising a
 CC sequence that binds an immunoglobulin Fc region. The polypeptides are
 CC useful as binding molecules for detecting, isolating or purifying
 CC immunoglobulin Fc-region polypeptides present in a solution, e.g. whole
 CC blood, plasma or transgenic milk. The Fc-region binding polypeptides are
 CC also useful for regulating or preventing an antibody response, or for
 CC increasing the half-life and over all stability of a therapeutic or
 CC diagnostic compound that is administered to or enters the circulatory
 CC system of an individual. This sequence represents an Fc region binding
 CC peptide of the invention
 XX
 SQ Sequence 13 AA;
 Query Match 79.6%; Score 43; DB 6; Length 13;
 Best Local Similarity 62.5%; Pred. No. 5.2;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GYWLTIWG 8
 |||| :||

Db 1 GYCNVWG 8

RESULT 4
ADJ50760
ID ADJ50760 standard; peptide; 13 AA.
XX AC
XX ADJ50760;
XX DT
XX 06-MAY-2004 (first entry)
XX DE Human serum albumin binding peptide, Seq ID No 297.
XX KW human serum albumin; HSA; serum; blood; tumour; human.
XX OS Homo sapiens.
XX PN WO2003106493-A1.
XX PD 24-DEC-2003.
XX PF 16-JUN-2003; 2003WO-US018896.
XX PR 14-JUN-2002; 2002US-0388642P.
XX PA (DYAX-) DYAX CORP.
XX PI Sato AK, Dawson BM;
XX WPI; 2004-082161/08.
XX
XX Evaluating sample comprising soluble serum protein by forming complex
PT comprising serum protein and physically associated compounds using
PT peptide ligand that specifically binds with proteins, which is separated
PT and evaluated.
XX
XX Disclosure; SEQ ID NO 297; 191pp; English.
XX
XX The invention relates to a method of evaluating sample by providing a
CC soluble serum protein (I), one or more compounds physically associated
CC with (I), and a (I)-binding agent that comprises a peptide that
CC specifically binds to (I), allowing the (I)-binding agent to bind to (I)
CC to form a complex including one or more compounds physically associated
CC with (I), separating the complex from one or more components of the
CC sample, and evaluating one or more of the physically associated
CC compounds. The sample comprises blood or serum, or is obtained from a
CC biopsy. The sample may also be obtained from a tumour or a region within
CC 5 mm of a tumour. The method is useful for detecting modulators that
CC modulate interaction of serum protein-binding compound and serum protein
CC and for identifying binding ligands for serum protein. The present
CC sequence represents a serum albumin-binding peptide identified using the
CC method of the invention.
XX
XX Sequence 13 AA;
SQ
Query Match 79.6%; Score 43; DB 8; Length 13;
Best Local Similarity 62.5%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GYWLTIW 8
Db 1 GYCNVWG 8
RESULT 5
ABU30004
ID ABU30004 standard; protein; 474 AA.
XX AC
XX AC ABU30004;
XX DT
XX 19-JUN-2003 (first entry)
XX DE Protein encoded by prokaryotic essential gene #15531.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Enterococcus faecium.
XX WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX N-PSDB; ACA3387A.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 57928; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 474 AA;
SQ
Query Match 79.6%; Score 43; DB 6; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GYWLTIW 7
Db 94 GYWLTCW 100

```
RESULT 6
ADC97318
ID ADC97318 standard; protein; 492 AA.
XX
XX ADC97318;
AC
XX
XX 01-JAN-2004 (first entry)
DT
XX
XX E. faecium protein sequence SEQ ID 6945.
DE
XX
XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
KW
XX
XX Enterococcus faecium.
OS
XX
XX US6583275-B1.
PN
XX
XX 24-JUN-2003.
PD
XX
XX 30-JUN-1998; 98US-00107532.
PF
XX
XX 02-JUL-1997; 97US-0051571P.
PR
XX 14-MAY-1998; 98US-0085598P.
PR
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Doucette-Stamm LA, Bush D;
XX
XX WPI; 2003-799836/75.
PI
XX
XX N-PSDB; ADC93664.
DR
XX
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX
XX Example 1; SEQ ID NO 6945; 243pp; English.
PS
XX
XX The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridizing to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids is useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.
XX
XX Sequence 492 AA;
Query Match 79.6%; Score 43; DB 7; Length 492;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYWLTIW 7
DB 112 GYWLTCW 118
RESULT 7
AAB62747
ID AAB62747 standard; protein; 120 AA.
XX
XX
```

```
AC AAB62747;
XX
XX 03-APR-2001 (first entry)
XX
XX Human HIV-1 monoclonal antibody SEQ ID NO: 46.
DE
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis.
KW
XX
XX Homo sapiens.
OS
XX WO200100678-A1.
XX PN
XX 04-JAN-2001.
XX PD
XX 23-JUN-2000; 2000WO-US017327.
XX PF
XX 30-JUN-1999; 99US-0141701P.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Watkins BA, Reitz MS;
XX PI
XX WPI; 2001-112438/12.
XX DR
XX N-PSDB; AAF29048.
XX DR
XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.
XX
XX Claim 1; Page 51-52; 81pp; English.
PS
XX
XX The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection
XX
XX Sequence 120 AA;
Query Match 77.8%; Score 42; DB 4; Length 120;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYWLTIWG 8
DB 104 GYWVSYG 111
RESULT 8
AAB09365
ID AAB09365 standard; protein; 1140 AA.
XX
XX AAE09365;
AC
XX 19-NOV-2001 (first entry)
DT
XX
XX Human ATP-binding cassette transporter ABCC6, MRP6 truncated mutant.
DE
XX
XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; mutein.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX WO200162977-A2.
XX PN
XX 30-AUG-2001.
XX PD
XX 23-FEB-2001; 2001WO-US005741.
XX PF
```

```

XX PR 23-FEB-2000; 2000US-0184269P.
XX PA (PXEI-) PXE INT INC.
XX PA (UYHA-) UNIV HAWAII.
XX PI Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
XX DR WPI; 2001-536645/59.
XX DR N-PSDB; AAD16258.
XX PT Screening presence of Pseudoxanthoma elasticum mutation useful for
XX PT identifying homozygotes, compound heterozygotes or carriers involves
XX PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX PS Claim 10; Page; 163pp; English.
XX CC The invention relates to methods and compositions for diagnosing and
XX CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
XX CC dysfunctions. The invention is useful for screening for the presence of a
XX CC PXE mutation. Mutations associated with PXE maps to the ATP-binding
XX CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
XX CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
XX CC protein located in the plasma membrane containing 17 membrane- spanning
XX CC helices grouped into three transmembrane domains. PXE is inherited as an
XX CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
XX CC a heritable disorder characterised by mineralisation of elastic fibers in
XX CC skin, arteries and the retina, that result in dermal lesions with
XX CC associated laxity and loss of elasticity, arterial insufficiency,
XX CC cardiovascular disease and retinal haemorrhages leading to macular
XX CC degeneration. The method is useful for screening a population of
XX CC individuals in order to identify individuals with one or more PXE
XX CC associated MRP6 alleles who are then provided with appropriate genetic
XX CC counselling in view of the PXE status. The methods are useful for
XX CC identifying homozygotes, compound heterozygotes or carriers and thus are
XX CC useful in the area of genetic testing, carrier detection and prenatal
XX CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
XX CC transporter, ABCC6 (MRP6) truncated mutant which is obtained as the
XX CC result of a stop codon at position 1141 of MRP6 protein. Note: The
XX CC present sequence is not shown in the specification but is derived from
XX CC human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO:
XX CC 3] shown in figure 3 of the specification (AAE09361)
XX SQ Sequence 1140 AA;

Query Match 77.8%; Score 42; DB 4; Length 1140;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 965 GYWLTLW 971
||||:|

RESULT 9
AAE09362
ID AAE09362 standard; protein; 1498 AA.
XX AC AAE09362;
XX 19-NOV-2001 (first entry)
XX DT
XX DE Mouse ATP-binding cassette transporter ABCC6 (MRP6) protein.
XX KW Mouse; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
XX KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
XX KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
XX KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
XX XX
XX OS Mus musculus.
XX XX
XX PN W0200162977-A2.
XX FT

30-AUG-2001.
23-FEB-2001; 2001WO-US005741.
23-FEB-2000; 2000US-0184269P.
(PXEI-) PXE INT INC.
(UYHA-) UNIV HAWAII.
Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
WPI; 2001-536645/59.
N-PSDB; AAD16236.
Screening presence of Pseudoxanthoma elasticum mutation useful for
identifying homozygotes, compound heterozygotes or carriers involves
determining presence of mutation in MRP6 (ABCC6) nucleic acid.
Example 5; Page 152-159; 163pp; English.
The invention relates to methods and compositions for diagnosing and
treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
dysfunctions. The invention is useful for screening for the presence of a
PXE mutation. Mutations associated with PXE maps to the ATP-binding
cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
protein located in the plasma membrane containing 17 membrane- spanning
helices grouped into three transmembrane domains. PXE is inherited as an
autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
a heritable disorder characterised by mineralisation of elastic fibers in
skin, arteries and the retina, that result in dermal lesions with
associated laxity and loss of elasticity, arterial insufficiency,
cardiovascular disease and retinal haemorrhages leading to macular
degeneration. The method is useful for screening a population of
individuals in order to identify individuals with one or more PXE
associated MRP6 alleles who are then provided with appropriate genetic
counselling in view of the PXE status. The methods are useful for
identifying homozygotes, compound heterozygotes or carriers and thus are
useful in the area of genetic testing, carrier detection and prenatal
diagnosis. The present sequence is mouse ATP-binding cassette (ABC)
transporter, ABCC6 (MRP6) protein belonging to sub-family 1C". Since
ABCC6 protein is involved in drug-resistance it is also called Multidrug
Resistance associated protein 6 (MRP6)
SQ Sequence 1498 AA;

Query Match 77.8%; Score 42; DB 4; Length 1498;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 960 GYWLTLW 966
||||:|

RESULT 10
AAY43544
ID AAY43544 standard; protein; 1503 AA.
XX AC AAY43544;
XX 26-JAN-2000 (first entry)
XX DT
XX DE A human MPR-related ABC transporter designated MOAT-E.
XX KW Human; MPR-related ABC transporter; MOAT protein; MOAT-E;
XX KW MOAT mediated transport; anticancer drug sensitivity;
XX KW transporter mediated cellular efflux; anticancer.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1215

```


DT 19-NOV-2001 (first entry)
DE Human ATP-binding cassette transporter ABCG6 (MRP6) R1314W mutant.
XX
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCG6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; mutin.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1314
FT /note= "Wild type Arg substituted with Trp"
XX
XX WO200162977-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US005741.
XX
XX 23-FEB-2000; 2000US-0184269P.
XX
XX (PXE1-) PXE INT INC.
XX (UYHA-) UNIV HAWAII.
XX
XX Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
XX
XX WPI; 2001-536645/59.
XX N-PSDB; AAD16263.
XX
XX Screening presence of Pseudoxanthoma elasticum mutation useful for
XX identifying homozygotes, compound heterozygotes or carriers involves
XX determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
XX Claim 13; Page; 163pp; English.
XX
XX The invention relates to methods and compositions for diagnosing and
XX treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
XX dysfunctions. The invention is useful for screening for the presence of a
XX PXE mutation. Mutations associated with PXE maps to the ATP-binding
XX cassette transporter ABCG6 (MRP6-Multidrug Resistance associated protein-
XX 6) gene locus on chromosome 16. ABCG6 (MRP6) gene encodes a 165 kDa
XX protein located in the plasma membrane containing 17 membrane- spanning
XX helices grouped into three transmembrane domains. PXE is inherited as an
XX autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
XX a heritable disorder characterised by mineralisation of elastic fibers in
XX skin, arteries and the retina, that result in dermal lesions with
XX associated laxity and loss of elasticity, arterial insufficiency,
XX cardiovascular disease and retinal haemorrhages leading to macular
XX degeneration. The method is useful for screening a population of
XX individuals in order to identify individuals with one or more PXE
XX associated MRP6 alleles who are then provided with appropriate genetic
XX counselling in view of the PXE status. The methods are useful for
XX identifying homozygotes, compound heterozygotes or carriers and thus are
XX useful in the area of genetic testing, carrier detection and prenatal
XX diagnosis. The present sequence is human ATP-binding cassette (ABC)
XX transporter, ABCG6 (MRP6) R1314W mutant protein. Note: The present
XX sequence is not shown in the specification but is derived from human ATP-
XX binding cassette transporter ABCG6 (MRP6) protein [SED ID NO: 3] shown in
XX figure 3 of the specification (AAE09361)
XX
XX Sequence 1503 AA;
XX
XX Query Match 77.8%; Score 42; DB 4; Length 1503;
XX Best Local Similarity 71.4%; Pred. No. 7.7e+02;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYWLTIW 7
Db 965 GYWLTLW 971

RESULT 13
AAE09367
ID AAE09367 standard; protein; 1503 AA.
XX
XX AAE09367;
XX
XX 19-NOV-2001 (first entry)
XX
XX Human ATP-binding cassette transporter ABCG6 (MRP6) V1298F mutant.
XX
XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
XX Multidrug Resistance-associated protein 6; macular degeneration; ABCG6;
XX ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
XX Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
XX mutant; mutin.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1298
FT /note= "Wild type Val substituted with Phe"
XX
XX WO200162977-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US005741.
XX
XX 23-FEB-2000; 2000US-0184269P.
XX
XX (PXE1-) PXE INT INC.
XX (UYHA-) UNIV HAWAII.
XX
XX Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
XX
XX WPI; 2001-536645/59.
XX N-PSDB; AAD16260.
XX
XX Screening presence of Pseudoxanthoma elasticum mutation useful for
XX identifying homozygotes, compound heterozygotes or carriers involves
XX determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
XX Claim 13; Page; 163pp; English.
XX
XX The invention relates to methods and compositions for diagnosing and
XX treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
XX dysfunctions. The invention is useful for screening for the presence of a
XX PXE mutation. Mutations associated with PXE maps to the ATP-binding
XX cassette transporter ABCG6 (MRP6-Multidrug Resistance associated protein-
XX 6) gene locus on chromosome 16. ABCG6 (MRP6) gene encodes a 165 kDa
XX protein located in the plasma membrane containing 17 membrane- spanning
XX helices grouped into three transmembrane domains. PXE is inherited as an
XX autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
XX a heritable disorder characterised by mineralisation of elastic fibers in
XX skin, arteries and the retina, that result in dermal lesions with
XX associated laxity and loss of elasticity, arterial insufficiency,
XX cardiovascular disease and retinal haemorrhages leading to macular
XX degeneration. The method is useful for screening a population of
XX individuals in order to identify individuals with one or more PXE
XX associated MRP6 alleles who are then provided with appropriate genetic
XX counselling in view of the PXE status. The methods are useful for
XX identifying homozygotes, compound heterozygotes or carriers and thus are
XX useful in the area of genetic testing, carrier detection and prenatal
XX diagnosis. The present sequence is human ATP-binding cassette (ABC)
XX transporter, ABCG6 (MRP6) V1298F mutant protein. Note: The present
XX sequence is not shown in the specification but is derived from human ATP-
XX binding cassette transporter ABCG6 (MRP6) protein [SED ID NO: 3] shown in
XX figure 3 of the specification (AAE09361)
XX
XX Sequence 1503 AA;

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Query Match          77.8%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 965 GYWLSLW 971

RESULT 14
ID AAE09368 standard; protein; 1503 AA.
XX
AC AAE09368;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human ATP-binding cassette transporter ABCC6 (MRP6) G1302R mutant.
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; munein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1302 /note= "Wild type Gly substituted with Arg"
XX
PN WO200162977-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005741.
XX
PR 23-FEB-2000; 2000US-0184269P.
XX
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
XX
PI Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
XX
DR WPI; 2001-536645/59.
DR N-PSDB; AAD16261.
XX
PT Screening presence of Pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
PS Claim 13; Page; 163pp; English.
XX
CC The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of a
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
CC protein located in the plasma membrane containing 17 membrane-spanning
CC helices grouped into three transmembrane domains. PXE is inherited as an
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
CC a heritable disorder characterised by mineralisation of elastic fibers in
CC skin, arteries and the retina, that result in dermal lesions with
CC associated laxity and loss of elasticity, arterial insufficiency,
CC cardiovascular disease and retinal haemorrhages leading to macular
CC degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are

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CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC
CC transporter, ABCC6 (MRP6) G1302R mutant protein. Note: The present
CC sequence is not shown in the specification but is derived from human ATP-
CC binding cassette transporter ABCC6 (MRP6) protein (SED ID NO: 3) shown in
CC figure 3 of the specification (AAE09361)
XX
SQ Sequence 1503 AA;

Query Match          77.8%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 965 GYWLSLW 971

RESULT 15
AAE09369
ID AAE09369 standard; protein; 1503 AA.
XX
AC AAE09369;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human ATP-binding cassette transporter ABCC6 (MRP6) A1303P mutant.
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; munein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1303 /note= "Wild type Ala substituted with Pro"
XX
PN WO200162977-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005741.
XX
PR 23-FEB-2000; 2000US-0184269P.
XX
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
XX
PI Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
XX
DR WPI; 2001-536645/59.
DR N-PSDB; AAD16262.
XX
PT Screening presence of Pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
PS Claim 13; Page; 163pp; English.
XX
CC The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of a
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
CC protein located in the plasma membrane containing 17 membrane-spanning
CC helices grouped into three transmembrane domains. PXE is inherited as an
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
CC a heritable disorder characterised by mineralisation of elastic fibers in

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CC skin, arteries and the retina, that result in dermal lesions with
CC associated laxity and loss of elasticity, arterial insufficiency,
CC cardiovascular disease and retinal haemorrhages leading to macular
CC degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABCG6 (MRP6) A1303P mutant protein. Note: The present
CC sequence is not shown in the specification but is derived from human ATP-
CC binding cassette transporter ABCG6 (MRP6) protein [SED ID NO: 3] shown in
CC figure 3 of the specification (AAE09361)
XX
SQ Sequence 1503 AA;

Query Match 77.8%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Fred. NO. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYMLTIW 7
|||:|
Db 965 GYMLSLW 971

Search completed: January 3, 2005, 12:09:53
Job time : 153 secs

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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:06:49 ; Search time 38 Seconds
(without alignments)
13.962 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywltiwg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 43 | 79.6 | 492 | 4 | US-09-107-532A-6945 |
| 2 | 42 | 77.8 | 1498 | 4 | Sequence 9, Appli |
| 3 | 42 | 77.8 | 1503 | 4 | Sequence 3, Appli |
| 4 | 41 | 75.9 | 222 | 4 | US-09-071-035-408 |
| 5 | 41 | 75.9 | 229 | 4 | Sequence 408, App |
| 6 | 41 | 75.9 | 266 | 4 | US-09-134-000C-3630 |
| 7 | 40 | 74.1 | 688 | 4 | Sequence 3630, Ap |
| 8 | 39 | 72.2 | 478 | 4 | US-09-071-035-406 |
| 9 | 38 | 70.4 | 328 | 4 | Sequence 406, App |
| 10 | 37 | 68.5 | 24 | 4 | US-09-248-796A-19350 |
| 11 | 37 | 68.5 | 12 | 4 | Sequence 19350, A |
| 12 | 37 | 68.5 | 132 | 4 | Sequence 6868, Ap |
| 13 | 37 | 68.5 | 278 | 4 | Sequence 2629, Ap |
| 14 | 37 | 68.5 | 278 | 4 | Sequence 41173, A |
| 15 | 37 | 68.5 | 499 | 4 | Sequence 56389, A |
| 16 | 37 | 68.5 | 591 | 4 | Sequence 22785, A |
| 17 | 37 | 68.5 | 591 | 4 | Sequence 11, Appl |
| 18 | 37 | 68.5 | 865 | 4 | Sequence 18, Appl |
| 19 | 36.5 | 67.6 | 612 | 4 | Sequence 2328, A |
| 20 | 36 | 66.7 | 119 | 2 | Sequence 18, Appl |
| 21 | 36 | 66.7 | 119 | 4 | Sequence 18, Appl |
| 22 | 36 | 66.7 | 172 | 4 | Sequence 19339, A |
| 23 | 36 | 66.7 | 219 | 3 | Sequence 19134, A |
| 24 | 36 | 66.7 | 242 | 4 | Sequence 5, Appli |
| 25 | 36 | 66.7 | 247 | 4 | Sequence 5, Appli |
| 26 | 36 | 66.7 | 280 | 2 | US-09-107-532A-6560 |
| 27 | 36 | 66.7 | 280 | 1 | Sequence 52, Appl |

| | | | | | | |
|----|----|------|------|---|----------------------|-------------------|
| 28 | 36 | 66.7 | 367 | 4 | US-09-248-796A-15188 | Sequence 15188, A |
| 29 | 36 | 66.7 | 1528 | 1 | US-08-463-092B-6 | Sequence 6, Appli |
| 30 | 36 | 66.7 | 1528 | 2 | US-08-462-109A-6 | Sequence 6, Appli |
| 31 | 36 | 66.7 | 1528 | 3 | US-08-460-907B-6 | Sequence 6, Appli |
| 32 | 36 | 66.7 | 1528 | 3 | US-08-463-179A-6 | Sequence 6, Appli |
| 33 | 36 | 66.7 | 1528 | 3 | US-08-461-384B-6 | Sequence 6, Appli |
| 34 | 36 | 66.7 | 1531 | 1 | US-08-141-893-2 | Sequence 2, Appli |
| 35 | 36 | 66.7 | 1531 | 1 | US-08-463-092B-2 | Sequence 2, Appli |
| 36 | 36 | 66.7 | 1531 | 1 | US-08-463-092B-4 | Sequence 4, Appli |
| 37 | 36 | 66.7 | 1531 | 2 | US-08-462-109A-2 | Sequence 2, Appli |
| 38 | 36 | 66.7 | 1531 | 2 | US-08-462-109A-4 | Sequence 4, Appli |
| 39 | 36 | 66.7 | 1531 | 2 | US-08-460-907B-2 | Sequence 2, Appli |
| 40 | 36 | 66.7 | 1531 | 2 | US-08-460-907B-4 | Sequence 4, Appli |
| 41 | 36 | 66.7 | 1531 | 3 | US-08-463-179A-2 | Sequence 2, Appli |
| 42 | 36 | 66.7 | 1531 | 3 | US-08-463-179A-4 | Sequence 4, Appli |
| 43 | 36 | 66.7 | 1531 | 3 | US-08-461-384B-2 | Sequence 2, Appli |
| 44 | 36 | 66.7 | 1531 | 3 | US-08-461-384B-4 | Sequence 4, Appli |
| 45 | 36 | 66.7 | 1531 | 3 | US-08-407-207A-2 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-09-107-532A-6945
; Sequence 6945, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6945:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...492
; SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945

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Query Match          79.6%; Score 43; DB 4; Length 492;
Best Local Similarity 85.4%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
      |||||
Db      112 GYWLTCW 118

RESULT 2
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; TITLE OF INVENTION: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match          77.8%; Score 42; DB 4; Length 1498;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
      |||||
Db      960 GYWLSLW 966

RESULT 3
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; TITLE OF INVENTION: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match          77.8%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
      |||||
Db      965 GYWLSLW 971

RESULT 4
US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
```

```
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-408
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```
Query Match          75.9%; Score 41; DB 4; Length 222;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 GYWLTIW 8
      |||||
Db      179 GYWLTIW 186
```

```
RESULT 5
US-09-134-000C-3630
; Sequence 3630, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3630
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3630
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Query Match          75.9%; Score 41; DB 4; Length 229;
Best Local Similarity 62.5%; Pred. No. 61;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      1 GYWLTIW 8
```

```

; LENGTH: 668
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19350

Query Match 74.1%; Score 40; DB 4; Length 668;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWLTIW 7
Db 372 YWMTIW 377

RESULT 8
US-09-107-532A-6868
; Sequence 6868, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6868:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...478
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:

US-09-107-532A-6868

Query Match 72.2%; Score 39; DB 4; Length 478;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 98 GYWLSAW 104

```

```
RESULT 9
US-09-540-236-2629
; Sequence 2629, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2629
; LENGTH: 328
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2629

Query Match      70.4%; Score 38; DB 4; Length 328;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
Db      116 GQWLTW 122

RESULT 10
US-09-270-767-41173
; Sequence 41173, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41173
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-41173

Query Match      68.5%; Score 37; DB 4; Length 24;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWLTIWG 8
Db      16 HWLSLWG 22

RESULT 11
US-09-270-767-56389
; Sequence 56389, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56389
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56389

Query Match      68.5%; Score 37; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
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Query Match      68.5%; Score 37; DB 4; Length 24;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWLTIWG 8
Db      16 HWLSLWG 22

RESULT 12
US-09-248-796A-22785
; Sequence 22785, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22785
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (6),(77),(85)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-22785

Query Match      68.5%; Score 37; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWLTI 6
Db      123 GYWLTI 128

RESULT 13
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.O1
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match      68.5%; Score 37; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
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Job time : 39 secs

Db 108 GYWIFLW 114
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RESULT 14
US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match 68.5%; Score 37; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
|||: :|
Db 108 GYWIFLW 114

RESULT 15
US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328

Query Match 68.5%; Score 37; DB 4; Length 499;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
|||: :|
Db 111 GYWISAW 117

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:13:15 ; Search time 142 Seconds
(without alignments)
20.266 Million cell updates/sec

Title: SEQ32

Perfect score: 54

Sequence: 1 gywltiwg 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 54 | 100.0 | 10 | 13 | US-10-046-922-34 |
| 2 | 54 | 100.0 | 10 | 13 | US-10-046-922-35 |
| 3 | 43 | 79.6 | 13 | 14 | US-10-125-869A-73 |
| 4 | 43 | 79.6 | 13 | 15 | US-10-462-262-297 |
| 5 | 43 | 79.6 | 474 | 15 | US-10-282-122A-57928 |
| 6 | 43 | 79.6 | 671 | 16 | US-10-437-963-190740 |
| 7 | 42 | 77.8 | 1498 | 10 | US-09-792-616-9 |
| 8 | 42 | 77.8 | 1498 | 16 | US-10-764-328-9 |
| 9 | 42 | 77.8 | 1503 | 10 | US-09-792-616-3 |
| 10 | 42 | 77.8 | 1503 | 16 | US-10-764-328-3 |
| 11 | 41 | 75.9 | 14 | 14 | US-10-125-869A-114 |
| 12 | 41 | 75.9 | 14 | 15 | US-10-462-262-338 |
| 13 | 41 | 75.9 | 34 | 9 | US-09-864-761-43458 |

Sequence 240891, Sequence 408, App Sequence 408, App Sequence 406, App Sequence 406, App Sequence 194869, Sequence 1, Appli Sequence 5, Appli Sequence 9, Appli Sequence 13, Appli Sequence 17, Appli Sequence 21, Appli Sequence 25, Appli Sequence 29, Appli Sequence 33, Appli Sequence 37, Appli Sequence 41, Appli Sequence 43, Appli Sequence 86, Appli Sequence 90, Appli Sequence 8834, Ap Sequence 75, Appli Sequence 299, App Sequence 226815, Sequence 188067, Sequence 13764, A Sequence 5178, Ap Sequence 88, Appli Sequence 52805, A Sequence 57680, A Sequence 4579, Ap Sequence 260407, Sequence 240891, Sequence 408, App Sequence 408, App Sequence 406, App Sequence 406, App Sequence 194869, Sequence 1, Appli Sequence 5, Appli Sequence 9, Appli Sequence 13, Appli Sequence 17, Appli Sequence 21, Appli Sequence 25, Appli Sequence 29, Appli Sequence 33, Appli Sequence 37, Appli Sequence 41, Appli Sequence 43, Appli Sequence 86, Appli Sequence 90, Appli Sequence 8834, Ap Sequence 75, Appli Sequence 299, App Sequence 226815, Sequence 188067, Sequence 13764, A Sequence 5178, Ap Sequence 88, Appli Sequence 52805, A Sequence 57680, A Sequence 4579, Ap Sequence 260407,

ALIGNMENTS

RESULT 1

US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match 100.0%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8

Db 2 GYWLTIWG 9

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RESULT 2
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Ekki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match      100.0%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWLTIWG 8
DB      2 GYWLTIWG 9

RESULT 3
US-10-125-869A-73
; Sequence 73, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-73

Query Match      79.6%; Score 43; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYWLTIWG 8
DB      1 GYWCNVWG 8

RESULT 4
US-10-462-262-297
; Sequence 297, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; APPLICANT:

; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-297

Query Match      79.6%; Score 43; DB 15; Length 13;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYWLTIWG 8
DB      1 GYWCNVWG 8

RESULT 5
US-10-282-122A-57928
; Sequence 57928, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57928
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Enterococcus faecium
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US-10-282-122A-57928

Query Match 79.6%; Score 43; DB 15; Length 474;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
|||
Db 94 GYWLTCW 100

RESULT 6

US-10-437-963-190740
; Sequence 190740, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190740
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87125C.1.pcp
US-10-437-963-190740

Query Match 79.6%; Score 43; DB 16; Length 671;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWLTIWG 8
|||
Db 329 YWTTIWG 335

RESULT 7

US-09-792-616-9
; Sequence 9, Application US/09792616
; Publication No. US20030165828A1
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match 77.8%; Score 42; DB 10; Length 1498;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
|||
|||

Db 960 GYWLSLW 966

RESULT 8

US-10-764-328-9
; Sequence 9, Application US/10764328
; Publication No. US20040166521A1
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001PC
; CURRENT APPLICATION NUMBER: US/10/764,328
; CURRENT FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-764-328-9

Query Match 77.8%; Score 42; DB 16; Length 1498;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7

|||
Db 960 GYWLSLW 966

RESULT 9

US-09-792-616-3
; Sequence 3, Application US/09792616
; Publication No. US20030165828A1
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match 77.8%; Score 42; DB 10; Length 1503;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7

|||
Db 965 GYWLSLW 971

RESULT 10

US-10-764-328-3
; Sequence 3, Application US/10764328
; Publication No. US20040166521A1
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001PC
; CURRENT APPLICATION NUMBER: US/10/764,328
; CURRENT FILING DATE: 2004-01-23

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-328-3

Query Match      77.8%; Score 42; DB 16; Length 1503;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
      |||||:|
Db      965 GYWLSLW 971

RESULT 11
US-10-125-869A-114
; Sequence 114, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-114

Query Match      75.9%; Score 41; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYWLTIWG 8
      |:|:|
Db      1 GFWCTFWG 8

RESULT 12
US-10-462-262-338
; Sequence 338, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAP TO AC000403.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-262-338

Query Match      75.9%; Score 41; DB 15; Length 14;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYWLTIWG 8
      |:|:|
Db      1 GFWCTFWG 8

RESULT 13
US-09-864-761-43458
; Sequence 43458, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43458
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC000403.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
US-09-864-761-43458

Query Match 75.9%; Score 41; DB 9; Length 34;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIW 8
Db 25 GYWLTVG 32

RESULT 14

US-10-424-599-240891
; Sequence 240891, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240891
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(82)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59551C.1.pep
US-10-424-599-240891

Query Match 75.9%; Score 41; DB 15; Length 82;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
Db 76 GYWLNLW 82

RESULT 15

US-09-071-035-408
; Sequence 408, Application US/09071035
; Publication No. US20020045737A1
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-408

Query Match 75.9%; Score 41; DB 9; Length 222;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 8
Db 179 GTWLTLWG 186

Search completed: January 3, 2005, 12:25:21
Job time : 143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:03:34 ; Search time 38 Seconds
(without alignments)
20.256 Million cell updates/sec

Title: SEQ32

Perfect score: 54

Sequence: 1 gylwtiw 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 42 | 77.8 | 441 | 2 C95307 | probable transport |
| 2 | 42 | 77.8 | 1502 | 2 T42216 | multidrug resistanc |
| 3 | 41 | 75.9 | 391 | 2 PC4117 | replication protei |
| 4 | 41 | 75.9 | 419 | 2 E30446 | permease (imported |
| 5 | 40 | 74.1 | 142 | 2 C34903 | Ig heavy chain pre |
| 6 | 40 | 74.1 | 425 | 2 B71038 | probable Na+/H+-ex |
| 7 | 40 | 74.1 | 508 | 2 C95282 | probable ABC trans |
| 8 | 39 | 72.2 | 376 | 2 AF1978 | hypothetical prote |
| 9 | 39 | 72.2 | 475 | 2 T46745 | arginine/ornithine |
| 10 | 39 | 72.2 | 490 | 2 C86879 | arginine/ornithine |
| 11 | 38 | 70.4 | 118 | 2 T35739 | probable integral |
| 12 | 38 | 70.4 | 426 | 2 C75176 | na+/h+ antiporter |
| 13 | 38 | 70.4 | 477 | 2 G90251 | ABCtransporter lim |
| 14 | 38 | 70.4 | 583 | 2 T50103 | probable oxidoredu |
| 15 | 38 | 70.4 | 829 | 2 S58888 | ins p4-binding pro |
| 16 | 38 | 70.4 | 829 | 2 S71847 | ins p4-binding pro |
| 17 | 37.5 | 69.4 | 1063 | 2 A33830 | cation efflux syst |
| 18 | 37.5 | 69.4 | 1063 | 2 JC4700 | cadmium, zinc, cob |
| 19 | 37 | 68.5 | 123 | 1 AVMS14 | Ig heavy chain v r |
| 20 | 37 | 68.5 | 167 | 2 AF0881 | probable exported |
| 21 | 37 | 68.5 | 172 | 2 A12232 | hypothetical prote |
| 22 | 37 | 68.5 | 187 | 1 S13868 | ubiquinol-cytochro |
| 23 | 37 | 68.5 | 197 | 2 AF2356 | hypothetical prote |
| 24 | 37 | 68.5 | 218 | 2 S76385 | hypothetical prote |
| 25 | 37 | 68.5 | 286 | 2 E88690 | protein F41H10.7 l |
| 26 | 37 | 68.5 | 292 | 2 S49164 | LysR-type protein |
| 27 | 37 | 68.5 | 360 | 2 S74751 | CDP-glucose 4,6-de |
| 28 | 37 | 68.5 | 380 | 2 S12839 | Ig heavy chain pre |
| 29 | 37 | 68.5 | 416 | 2 AF1127 | rod shape-determin |

probable amino aci
arginine/ornithine
arginine/ornithine
probable transcarb
hypothetical prote
phosphatidylglycer
partial probable m
hypothetical prote
1-acyl-sn-glycerol
1-acylglycerol-3-p
hypothetical prote
GP12 protein yea
hypothetical prote
hypothetical prote
YSD83 protein - ye
probable membrane

30 37 68.5 472 2 B83497
31 37 68.5 482 2 JH0110
32 37 68.5 497 2 G86878
33 36.5 67.6 607 2 F82966
34 36 66.7 164 2 F69990
35 36 66.7 171 2 B83140
36 36 66.7 239 2 H85756
37 36 66.7 241 2 G82391
38 36 66.7 247 2 G81013
39 36 66.7 247 2 A81957
40 36 66.7 250 2 A69843
41 36 66.7 280 2 S61111
42 36 66.7 292 2 A83779
43 36 66.7 351 2 D84541
44 36 66.7 385 2 S43540
45 36 66.7 387 2 B90862

RESULT 1
C95307
Probable transport protein SMA0684 [imported] - Sinorhizobium meliloti (strain 1021) mag
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95307
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95307
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <KUR>
A:Cross-references: UNIPROT:Q92ZT6; GB:AB006469; PIDN:AAK65021.1; PID:gl4523451; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 568-572, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMA0684
A:Genome: plasmid
C:Superfamily: L-lysine transport protein

Query Match 77.8%; Score 42; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYMLTIW 7
Db 92 GYWSIW 98

RESULT 2
T42216
multidrug resistance-associated protein homolog MLP-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42216
R:Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A:Title: Hepatic expression of multidrug resistance-associated protein-like proteins mai
A:Reference number: Z22081; MUID:98279126; PMID:9614210
A:Accession: T42216
A>Status: preliminary; translated from GB/EMBL/DBJ

ALIGNMENTS

A;Molecule type: mRNA
A;Residues: 1-1502 <HIR>
A;Cross-references: UNIPROT:O88269; EMBL:AB010466; NID:G3242457; PIDN:BAA28954.1; PID:93
A;Experimental source: Strain Sprague-Dawley; liver
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 77.8%; Score 42; DB 2; Length 1502;
Best Local Similarity 71.4%; Pred. No. 18+02; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0;

QY 1 GYWLTIW 7
| | | | |
Db 964 GYWLSLW 970

RESULT 3
PC4117
replication protein homolog - Pyrococcus sp. (fragment)
N;Alternate names: hypothetical 391 protein
C;Species: Pyrococcus sp.
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 17-May-1996
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.
A;Reference number: JC4514; MUID:96105215; PMID:8529878
A;Accession: PC4117
A;Molecule type: DNA
A;Residues: 1-391 <RAS>
A;Cross-references: DDBJ:D50018

Query Match 75.9%; Score 41; DB 2; Length 391;
Best Local Similarity 85.7%; Pred. No. 41; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1;

QY 2 YWLTIWG 8
| | | | |
Db 155 YWLTEWG 161

RESULT 4
E90446
permease [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90446
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <KUR>
A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:gl3816037; PIDN:AAK42828.1; GSPDB:G
C;Genetics:
A;Gene: SSO2718

Query Match 75.9%; Score 41; DB 2; Length 419;
Best Local Similarity 62.5%; Pred. No. 43; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1;

QY 1 GYWLTIWG 8
| | | | |
Db 365 GFWEITLWG 372

RESULT 5
C34903
Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
C;Accession: C34903
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-react
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: C34903
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-142 <BED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;34-119/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 142;
Best Local Similarity 62.5%; Pred. No. 22; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 3;

QY 1 GYWLTIWG 8
| | | | |
Db 126 GYWFAYWG 133

RESULT 6
B71038
probable Na+/H+-exchanging protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: B71038
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: B71038
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-425 <KAW>
A;Cross-references: UNIPROT:O59255; GB:AP000006; NID:G3236133; PIDN:BAA30706.1; PID:G3255
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1594

Query Match 74.1%; Score 40; DB 2; Length 425;
Best Local Similarity 75.0%; Pred. No. 63; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 2;

QY 1 GYWLTIWG 8
| | | | |
Db 319 GAWLTAWG 326

RESULT 7
C95282
probable ABC transporter, periplasmic solute-binding protein, family 5 Sma0302 [imported]
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95282
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, P.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95282
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-508 <KUR>
A;Cross-references: UNIPROT:Q930N2; GB:AE006469; PIDN:AAK64821.1; PID:gl4523232; GSPDB:G
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0302
A:Genome: plasmid

Query Match 74.1%; Score 40; DB 2; Length 508;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
|||:|
Db 393 GYWTIW 399

RESULT 8
AF1978
hypothetical protein alr1377 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF1978
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF1978
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <KUR>
A:Cross-references: UNIPROT:Q8YX40; GB:BA000019; PIDN:BA073334.1; PID:gl17130724; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1377

Query Match 72.2%; Score 39; DB 2; Length 376;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYWLTIW 8
|||:|
Db 124 GEWLRWG 131

RESULT 9
T46745
arginine/ornithine antiporter [imported] - *Lactobacillus sakei*
C:Species: *Lactobacillus sakei*
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T46745
R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, J. Bacteriol. 180, 4154-4159, 1998
A:Title: Structural and functional analysis of the gene cluster encoding the enzymes of
A:Reference number: 223141; MUID:98361904; PMID:9696763
A:Accession: T46745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <ZUN>
A:Cross-references: UNIPROT:O53092; EMBL:AJ001330; NID:g2764610; PIDN:CAA04686.1; PID:g2
C:Genetics:
A:Gene: arcB
C:Function:
A:Description: necessary for arginine transport; involved in ornithine-arginine exchange
A:Pathway: arginine catabolism
C:Superfamily: L-lysine transport protein

Query Match 72.2%; Score 39; DB 2; Length 475;
Best Local Similarity 71.4%; Pred. No. 99;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
|||:|
Db 94 GYWLSAW 100

RESULT 10
C86879
arginine/ornithine antiporter [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL140
C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86879
R:Bolojin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s.s.
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <STO>
A:Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:gl2725084; PIDN:AAK06133.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: arcD1
C:Superfamily: L-lysine transport protein

Query Match 72.2%; Score 39; DB 2; Length 490;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
|||:|
Db 93 GYWLSAW 99

RESULT 11
T35739
probable integral membrane protein - *Streptomyces coelicolor*
C:Species: *Streptomyces coelicolor*
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35739
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. submitted to the EMBL Data Library, August 1999
A:Reference number: Z21588
A:Accession: T35739
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-118 <SAU>
A:Cross-references: UNIPROT:Q9S2K9; EMBL:AL109732; PIDN:CAB52050.1; GSPDB:GN00070; SCOE
C:Genetics:
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOE:SC7H2.08
C:Superfamily: *Streptomyces coelicolor* probable integral membrane protein SC7H2.08

Query Match 70.4%; Score 38; DB 2; Length 118;
Best Local Similarity 57.1%; Pred. No. 38;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWLTIW 8
|||:|
Db 51 FWLSLWG 57

RESULT 12
C75176
na+/h+ antiporter (napa-2) PAB0390 - *Pyrococcus abyssi* (strain Orsay)
C:Species: *Pyrococcus abyssi*
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C75176
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru

A;Reference number: A75001
A;Accession: C75176
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <RAW>
A;Cross-references: UNIPROT:Q9V160; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB4949
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: napA-2; PAB0390
C;Superfamily: Aquifex aeolicus Na⁺/H⁺-exchanging protein napA1

Query Match 70.4%; Score 38; DB 2; Length 426;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
|:|:|:|
Db 320 GAWITAWG 327

RESULT 13

G90251
ABCTransporter [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90251
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <KUR>
A;Cross-references: UNIPROT:Q97ZC3; GB:AE006641; NID:gl3814184; PIDN:AAK41270.1; GSPDB:G
C;Genetics:
A;Gene: S800999

Query Match 70.4%; Score 38; DB 2; Length 477;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WLTIWG 8
|:|:|:|
Db 415 WITWVG 420

RESULT 14

T50103
probable oxidoreductase [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50103
R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25038
A;Accession: T50103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-583 <SEE>
A;Cross-references: UNIPROT:Q9US28; EMBL:AL136499; PIDN:CAB66164.1; GSPDB:GN000066; SPDB:
A;Experimental source: strain 972h(-); cosmid c1783
C;Genetics:
A;Gene: SPDB:SPAC1783.01
A;Map position: 1

Query Match 70.4%; Score 38; DB 2; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8

Db 244 GRWPTIWG 251
|:|:|:|

RESULT 15

S58888
Ins P4-binding protein - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Apr-2004
R;Cullen, P.J.; Hsuan, J.J.; Truong, O.; Letcher, A.J.; Jackson, T.R.; Dawson, A.P.; Irvi-
Nature 376, 527-530, 1995
A;Title: Identification of a specific Ins(1,3,4,5)P(4)-binding protein as a member of the
A;Reference number: S58888; MUID:95364929; PMID:7637787
A;Accession: S58888
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-829 <CUL>
A;Cross-references: EMBL:X89399
F;328-539/Domain: ras-specific GAP catalytic domain homology <GAP>
F;571-670/Domain: pleckstrin repeat homology <PLK>

Query Match 70.4%; Score 38; DB 2; Length 829;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
|:|:|:|
Db 689 GHWLCCWG 696

Search completed: January 3, 2005, 12:13:50
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: January 3, 2005, 11:52:29 ; Search time 187 Seconds
(without alignments)
24.615 Million cell updates/sec

Title: SEQ32

Perfect score: 54

Sequence: 1 gywtiing 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 43 | 79.6 | 221 | 2 Q74JK6 | Q74jk6 lactobacill |
| 2 | 43 | 79.6 | 221 | 2 AAS08923 | Aas08923 lactobaci |
| 3 | 43 | 79.6 | 733 | 2 Q8H2N7 | Q8h2n7 oryza sativ |
| 4 | 42 | 77.8 | 284 | 2 Q6MCD1 | Q6mc01 parachlamyd |
| 5 | 42 | 77.8 | 284 | 2 CAF23898 | Caf23898 parachlam |
| 6 | 42 | 77.8 | 441 | 2 Q92ZT6 | Q92zt6 rhizobium m |
| 7 | 42 | 77.8 | 1308 | 2 Q8T6H2 | Q8t6h2 dictyosteli |
| 8 | 42 | 77.8 | 1498 | 1 MRP6_MOUSE | Q8r1e7 mus musculu |
| 9 | 42 | 77.8 | 1502 | 1 MRP6_RAT | Q88269 rattus norv |
| 10 | 42 | 77.8 | 1503 | 1 MRP6_HUMAN | Q95255 homo sapien |
| 11 | 41 | 75.9 | 266 | 2 Q82Z85 | Q82z85 enterococcu |
| 12 | 41 | 75.9 | 376 | 2 Q6CBE4 | Q6cbe4 yarrowia li |
| 13 | 41 | 75.9 | 413 | 2 Q9HKA9 | Q9hka9 thermoplasm |
| 14 | 41 | 75.9 | 419 | 2 Q97VB7 | Q97vb7 sulfolobus |
| 15 | 41 | 75.9 | 736 | 2 Q8DMV4 | Q8dmv4 synchococc |
| 16 | 41 | 75.9 | 1052 | 2 Q7YZ84 | Q7yz84 plasmodium |
| 17 | 41 | 75.9 | 1652 | 2 Q74DR3 | Q74dr3 geobacter s |
| 18 | 41 | 75.9 | 1652 | 2 AAR34628 | Aar34628 geobacter |
| 19 | 40 | 74.1 | 167 | 1 OB_MACMU | Q28504 macaca mula |
| 20 | 40 | 74.1 | 331 | 2 Q775C7 | Q775c7 bordetella |
| 21 | 40 | 74.1 | 331 | 2 AAR97683 | Aar97683 bordetell |
| 22 | 40 | 74.1 | 401 | 2 Q9KHQ6 | Q9khq6 bacteroides |
| 23 | 40 | 74.1 | 425 | 2 Q952S5 | Q952s5 pyrococcus |
| 24 | 40 | 74.1 | 508 | 2 Q930N2 | Q930n2 rhizobium m |
| 25 | 40 | 74.1 | 1970 | 2 Q88H71 | Q88h71 pseudomonas |
| 26 | 39 | 72.2 | 91 | 2 Q82A22 | Q82a22 streptomyce |
| 27 | 39 | 72.2 | 117 | 2 Q7S013 | Q7s013 neurospora |
| 28 | 39 | 72.2 | 144 | 2 Q6M566 | Q6m566 corynebacte |
| 29 | 39 | 72.2 | 144 | 2 CAF21531 | Caf21531 corynebac |
| 30 | 39 | 72.2 | 162 | 2 Q8NQ86 | Q8nqb6 corynebacte |
| 31 | 39 | 72.2 | 253 | 2 Q32816 | Q32816 lactococcus |

32 Q9ARZ0 oryza sativ
33 Q6C129 yarrowia li
34 Q8YX40 anabaena sp
35 Q8ZUS8 pyrobaculum
36 Q7NSJ2 chromobacte
37 Q9KGV3 lactococcus
38 Q6TK71 streptococc
39 Aar30325 streptoco
40 Q6HP27 bacillus th
41 Q73E85 bacillus ce
42 Q81IH9 bacillus ce
43 Aas39409
44 ARCD_LACSK
45 Q8DWP9 streptococc

ALIGNMENTS

RESULT 1

Q74JK6 PRELIMINARY; PRT; 221 AA.
AC Q74JK6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hemolysin-like protein.
GN OrderedLocusNames=LJ1101;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC533;
RX PubMed=14966310;
RA Priddy R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
Lactobacillus johnsonii NC533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017203; AAS08923.1;
DR InterPro; IPR004254; HlyIII-related.
DR InterPro; IPR005744; HlyIII.
DR Pfam; PF03006; HlyIII; 1.
DR TIGRFAMs; TIGR01065; hlyIII; 1.
KW Complete proteome.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 79.6%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWTIING 8

Db 172 GFWLLVWG 179

RESULT 2

AAS08923 PRELIMINARY; PRT; 221 AA.
AC AAS08923

DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Hemolysin-like protein.
GN Lj1101.

OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Priddy R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017203; AAS08923.1; -.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 79.6%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
Db 172 GFLLVWG 179

RESULT 3
Q8H2N7 ID Q8H2N7 PRELIMINARY; PRT; 733 AA.
AC Q8H2N7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein QJ1138_B05.118.
GN Names=QJ1138_B05.118;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005486; BAC16197.1; -.
DR Gramene; Q8H2N7; -.
DR InterPro; IPR007658; DUF594.
DR Pfam; PF04578; DUF594; 1.
KW Hypothetical protein.
SQ SEQUENCE 733 AA; 82939 MW; E95884DAD1DC2AC9 CRC64;

Query Match 79.6%; Score 43; DB 2; Length 733;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWLTWIG 8
Db 328 YWTTWIG 334

RESULT 4
Q6MC01 ID Q6MC01 PRELIMINARY; PRT; 284 AA.
AC Q6MC01;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=pc1174;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=null;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Drooge M., Frishman D.,
RA Rattei T., Mewes H.-W., Wagner M.;

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RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF23898.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;

Query Match 77.8%; Score 42; DB 2; Length 284;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWLTWIG 8
Db 273 YWLSLWG 279

RESULT 5
CAF23898 ID CAF23898 PRELIMINARY; PRT; 284 AA.
AC CAF23898;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN PC1174.
OS Parachlamydia sp. UWE25.
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UWE25;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Drooge M., Frishman D.,
RA Rattei T., Mewes H., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=UWE25;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Drooge M., Frishman D.,
RA Rattei T., Mewes H., Wagner M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF23898.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;

Query Match 77.8%; Score 42; DB 2; Length 284;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWLTWIG 8
Db 273 YWLSLWG 279

RESULT 6
Q922T6 ID Q922T6 PRELIMINARY; PRT; 441 AA.
AC Q922T6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable transport protein.
GN OrderedLocusNames=RA0363; ORFNames=SMA0684;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSYMA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Pederspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT *Sinorhizobium meliloti* pSymA megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21368234; PubMed=11474104;
 RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
 RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
 RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
 RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
 RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
 RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
 RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
 RA Maey D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
 RA Ramberger U., Surzycki R., Thebault P., Vandenbol M.,
 RA Vorhoelzer F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
 RT "The composite genome of the legume symbiont *Sinorhizobium meliloti*.";
 RL Science 293:668-672(2001).
 DR EMBL; AE007228; AAK65021.1; -.
 DR PIR; C95307; C95307.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005279; P: amino acid-polyamine transporter activity; IEA.
 DR GO; GO:0006865; P: amino acid transport; IEA.
 DR GO; GO:0006810; P: transport; IEA.
 DR InterPro; IPR002293; AA/permease.
 DR Pfam; PF00324; AA/permease; 1.
 KW Complete proteome; Plasmid; Transmembrane; Transport.
 SQ SEQUENCE 441 AA; 46277 MW; B6F5C9EC96011AD0 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 441;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
 |||:|
 Db 92 GYWISIW 98

RESULT 7
 Q8T6H2 PRELIMINARY; PRT; 1308 AA.
 AC Q8T6H2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ABC transporter ABC7.
 GN Name=abcC7;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ax4;
 RA Anjard C., Loomie W.F.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AF474339; AAL85710.1; -.
 DR HSSP; P08716; IMT0.
 DR DictyBase; DDB0201630; abcC7.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005524; F: ATP binding; IEA.
 DR GO; GO:0004009; F: ATP-binding cassette (ABC) transporter acti. . .; IEA.
 DR GO; GO:0000166; F: nucleotide binding; IEA.
 DR GO; GO:0006810; P: transport; IEA.

DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011527; ABC_membrane_1.
 DR InterPro; IPR01140; ABC_TM_transp.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS0929; ABC_TM1F; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
 KW ATP-binding.
 SQ SEQUENCE 1308 AA; 149576 MW; 336120AC8F73AC1 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 1308;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWLTIW 7
 |||||
 Db 764 YWLTIW 769

RESULT 8
 MRP6_MOUSE STANDARD; PRT; 1498 AA.
 ID MRP6_MOUSE
 AC Q9R1S7; Q80VB6;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6).
 DE Name=Abcc6; Synonyms=Mrp6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ddy; TISSUE=Liver;
 RA Morikawa A., Suzuki H., Hirohashi T., Sugiyama Y.;
 RT "Mus musculus mRNA for multidrug resistance-associated protein 6 (MRP6), complete cds.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 685-1498 FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP REVIEW.
 RX DOI=10.1038/mp.a002623.01;
 RA Beck C., Le Saux O., Varadi A., Boyd C.;
 RT "Abcc6,"
 RL (er) AfCS-Nature Molecule Pages (2004).

CC -!- FUNCTION: May participate directly in the active transport of
CC drugs into subcellular organelles or influence drug distribution
CC indirectly (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
CC
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CC
CC EMBL; AB028737; BAA83820.1; -.
CC EMBL; BC049980; AAH49980.1; -.
CC HSSP; Q03518; 1UJ7.
CC MGD; MGI:1351634; Abcc6.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001140; ABC_TM_transpt.
CC InterPro; IPR003439; ABC_TM_transpt.
CC InterPro; IPR005292; MRP_assoc.
CC Pfam; PF00664; ABC membrane; 2.
CC Pfam; PF00005; ABC_tran; 2.
CC ProDom; PD000006; ABC transporter; 1.
CC SMART; SM00382; AAA; 2.
CC TIGRFAMs; TIGR00957; MRP_assoc_pro; 1.
CC PROSITE; PS00929; ABC_TM1F; 2.
CC PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
CC PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
CC ATP-binding; Glycophorin; Repeat; Transmembrane; Transport.
KW DOMAIN 1 37
FT TRANSMEM 38 58
FT DOMAIN 59 78
FT TRANSMEM 79 99
FT DOMAIN 100 104
FT TRANSMEM 105 125
FT DOMAIN 126 137
FT TRANSMEM 138 155
FT DOMAIN 156 173
FT TRANSMEM 174 194
FT DOMAIN 195 300
FT TRANSMEM 301 321
FT DOMAIN 322 347
FT TRANSMEM 348 368
FT DOMAIN 369 424
FT TRANSMEM 425 445
FT DOMAIN 446 448
FT TRANSMEM 449 469
FT DOMAIN 470 531
FT TRANSMEM 532 552
FT DOMAIN 553 574
FT TRANSMEM 575 595
FT DOMAIN 596 934
FT TRANSMEM 935 955
FT DOMAIN 956 992
FT TRANSMEM 993 1013
FT DOMAIN 1014 1056
FT TRANSMEM 1057 1077
FT DOMAIN 1078 1078
FT TRANSMEM 1079 1099
FT DOMAIN 1100 1170
FT TRANSMEM 1171 1191
FT DOMAIN 1192 1193
FT TRANSMEM 1194 1214
FT DOMAIN 1215 1498
FT TRANSMEM 1499 1668
FT NP_BIND 661 668
FT NP_BIND 1294 1301
FT CARBOHYD 21 21
FT CARBOHYD 341 341
FT CONFLICT 706 706
A -> V (in Ref. 2).

FT CONFLICT 927 927 I -> T (in Ref. 2).
FT CONFLICT 1401 1401 H -> Q (in Ref. 2).
FT CONFLICT 1448 1448 L -> V (in Ref. 2).
FT CONFLICT 1477 1477 N -> S (in Ref. 2).
SQ SEQUENCE 1498 AA; 164788 MW; EFCFF33F0EEC813C CRC64;
Query Match 77.8%; Score 42; DB 1; Length 1498;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWLTIW 7
Db 960 GYWLTLW 966
RESULT 9
MRP6_RAT
ID MRP6_RAT STANDARD; PRT; 1502 AA.
AC O88269;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-
DE family C, member 6) (MRP-like protein-1) (MLP-1).
DE Name=Abcc6; Synonyms=Mrp6, Mlp1.
GN Rattus norvegicus (Rat)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=98279126; PubMed=9614210; Kume K., Shimizu T.,
RA Hirohashi T., Suzuki H., Ito K., Ogawa K., Meier P.J., Stieger B.,
RT "Hepatic expression of multidrug resistance-associated protein-like
RT proteins maintained in eisa hyperbilirubinemic rats.";
RL Mol. Pharmacol. 53:1068-1075(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=20159081; PubMed=10692506;
RA Madon J., Hagenbuch B., Landmann L., Meier P.J., Stieger B.,
RT "Transport function and hepatocellular localization of mrp6 in rat
RT liver.";
RL Mol. Pharmacol. 57:634-641(2000).
CC -!- FUNCTION: May participate directly in the active transport of
CC drugs into subcellular organelles or influence drug distribution
CC indirectly (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: High in liver and lower in duodenum and
CC kidney.
CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
CC
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CC
CC EMBL; AB010466; BAA28954.1; -.
CC EMBL; U73038; AAD12747.1; -.
CC PIR; T42216; T42216.
CC HSSP; P08716; 1MT0.
CC RGD; 620268; Abcc6.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001140; ABC_TM_transpt.
CC InterPro; IPR003439; ABC_TM_transpt.
CC InterPro; IPR005292; MRP_assoc.
CC Pfam; PF00664; ABC membrane; 2.
CC Pfam; PF00005; ABC_tran; 2.

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DR ProDom: PR000006; ABC transporter; 1.
DR SMART: SMO0382; AAA; 2.
DR TIGRFAMs: TIGR00957; MRP_assoc_pro; 1.
DR PROSITE: PS00929; ABC_TM1F; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE: PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Glycoprotein; Repeat; Transmembrane; Transport.
FT DOMAIN 5 37 Extracellular (By similarity).
FT TRANSMEM 38 58 1 (By similarity).
FT DOMAIN 59 78 Cytoplasmic (By similarity).
FT TRANSMEM 79 99 2 (By similarity).
FT DOMAIN 100 104 Extracellular (By similarity).
FT TRANSMEM 105 125 3 (By similarity).
FT DOMAIN 126 137 Cytoplasmic (By similarity).
FT TRANSMEM 138 155 4 (By similarity).
FT DOMAIN 156 173 Extracellular (By similarity).
FT TRANSMEM 174 194 5 (By similarity).
FT DOMAIN 195 300 Cytoplasmic (By similarity).
FT TRANSMEM 301 321 6 (By similarity).
FT DOMAIN 322 347 Extracellular (By similarity).
FT TRANSMEM 348 368 7 (By similarity).
FT DOMAIN 369 424 Cytoplasmic (By similarity).
FT TRANSMEM 425 445 8 (By similarity).
FT DOMAIN 446 448 Extracellular (By similarity).
FT TRANSMEM 449 469 9 (By similarity).
FT DOMAIN 470 531 Cytoplasmic (By similarity).
FT TRANSMEM 532 552 10 (By similarity).
FT DOMAIN 553 574 Extracellular (By similarity).
FT TRANSMEM 575 595 11 (By similarity).
FT DOMAIN 596 938 Cytoplasmic (By similarity).
FT TRANSMEM 939 959 12 (By similarity).
FT DOMAIN 960 996 Extracellular (By similarity).
FT TRANSMEM 997 1017 13 (By similarity).
FT DOMAIN 1018 1060 Cytoplasmic (By similarity).
FT TRANSMEM 1061 1081 14 (By similarity).
FT DOMAIN 1082 1082 Extracellular (By similarity).
FT TRANSMEM 1083 1103 15 (By similarity).
FT DOMAIN 1104 1174 Cytoplasmic (By similarity).
FT TRANSMEM 1175 1195 16 (By similarity).
FT DOMAIN 1196 1197 Extracellular (By similarity).
FT TRANSMEM 1198 1218 17 (By similarity).
FT DOMAIN 1219 1502 Cytoplasmic (By similarity).
FT DOMAIN 627 851 ABC transporter 1.
FT TRANSMEM 1264 1498 ABC transporter 2.
FT NP_BIND 661 668 ATP (Potential).
FT NP_BIND 1298 1305 ATP (Potential).
FT CARBOHYD 21 21 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1502 AA; 164995 MW; 539901B674747A28 CRC64;

Query Match 77.8%; Score 42; DB 1; Length 1502;
Best Local Similarity 71.4%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
Db 964 GYWLISLW 970

RESULT 10
MRP6_HUMAN
ID MRP6_HUMAN STANDARD; PRT; 1503 AA.
AC O95255; P78420; Q9UMZ7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-
DE family C, member 6) (Anthracycline resistance-associated protein)
DE Name=ABCC6; Synonyms=MRP6, ARA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9910722; PubMed=9892204;
RA Kool M., van der Linden M., de Haas M., Baas F., Borst P.;
RT "Expression of human MRP6, a homologue of the multidrug resistance
RT protein gene MRP1, in tissues and cancer cells.";
RL Cancer Res. 59:175-182(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from
RT human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99352020; PubMed=10424734;
RA Belinsky M.G., Kruh G.D.;
RT "MOAT-E (ARA) is a full-length MRP/cMOAT subfamily transporter
RT expressed in kidney and liver.";
RL Br. J. Cancer 80:1342-1349(1999).
RN [4]
RP FUNCTION, AND CHARACTERIZATION OF VARIANTS PXE PHE-1298; ARG-1302 AND
RP SER-1321.
RX MEDLINE=21988190; PubMed=11880368; DOI=10.1074/jbc.M110918200;
RA Iliag A., Urban Z., Seidl T.L., Le Saux O., Sinko E., Boyd C.D.,
RA Sarkadi B., Varadi A.;
RT "Loss of ATP-dependent transport activity in pseudoxanthoma elasticum-
RT associated mutants of human ABCC6 (MRP6).";
RL J. Biol. Chem. 277:16860-16867(2002).
RN [5]
RP REVIEW, AND VARIANT PXE PRO-455.
RX MEDLINE=21321623; PubMed=11427982; DOI=10.1016/S1471-4914(00)01869-4;
RA Utto J., Pulkkinen L., Ringpfeil F.;
RT "Molecular genetics of pseudoxanthoma elasticum: a metabolic disorder
RT at the environment-genome interface?";
RL Trends Mol. Med. 7:13-17(2001).
RN [6]
RP VARIANT GLN-1268.
RX MEDLINE=20374463; PubMed=10913334; DOI=10.1006/bbrc.2000.3101;
RA Germain D.P., Perdu J., Remones V., Jeunemaitre X.;
RT "Homozygosity for the R1268Q mutation in MRP6, the pseudoxanthoma
RT elasticum gene, is not disease-causing.";
RL Biochem. Biophys. Res. Commun. 274:297-301(2000).
RN [7]
RP VARIANT ARG-64.
RX MEDLINE=20514578; PubMed=11058917;
RX DOI=10.1002/1098-1004(200011)16:5<449::AID-HUMU24>3.0.CO;2-O;
RA Germain D.P., Perdu J., Remones V., Manzoni K., Jeunemaitre X.;
RT "Identification of two polymorphisms (c189G>C; c190T>C) in exon 2 of
RT the human MRP6 gene (ABCC6) by screening of pseudoxanthoma elasticum
RT patients: possible sequence correction?";
RL Hum. Mutat. 16:449-449(2000).
RN [8]
RP VARIANT PXE CYS-1339, AND VARIANT GLN-632.
RX MEDLINE=20408303; PubMed=10954200;
RA Struk B., Cai L., Zaech S., Ji W., Chung J., Lumsden A., Stumm M.,
RA Huber M., Schaen L., Kim C.-A., Goldsmith L.A., Viljoen D.,
RA Figuera L.E., Fuchs W., Munier F., Ramesar R., Hohl D., Richards R.,
RA Neldner K.H., Lindpaintner K.;
RT "Mutations of the gene encoding the transmembrane transporter protein
RT ABC-C5 cause pseudoxanthoma elasticum.";
RL J. Mol. Med. 78:282-286(2000).
RN [9]
RP VARIANTS PXE PRO-1114; GLN-1138 AND TRP-1314, AND VARIANT ALA-614.
RX MEDLINE=20296630; PubMed=10835642; DOI=10.1038/76102;
RA Le Saux O., Urban Z., Tschuch C., Ceiszar K., Baccheili B.,
RA Quaglino D., Pasquali-Ronchetti I., Pope F.M., Richards A., Terry S.,
RA Bercovitch L., de Paeppe A., Boyd C.D.;
RT "Mutations in a gene encoding an ABC transporter cause pseudoxanthoma

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RT elastin;".
RL Nat. Genet. 25:223-227(2000).
RN [10]
RP VARIANT PXE TRP-1138, AND VARIANT GLN-1268.
RX MEDLINE=20283940; PubMed10811882; DOI=10.1073/pnas.100041297;
RA Ringfeil F., Leubwohl M.G., Christiano A.M., Uitto J.;
RT "Pseudoxanthoma elasticum: mutations in the MRP6 gene encoding a
transmembrane ATP-binding cassette (ABC) transporter";
RL Proc. Natl. Acad. Sci. U.S.A. 97:6001-6006(2000).
RN [11]
RP VARIANTS PXE LYS-411; GLN-518; SER-568; PRO-673; GLN-765; PRO-1114;
RP TRP-1121; PRO-1138; ASP-1203; PHE-1298; ILE-1301; ARG-1302;
RP PRO-1303; GLN-1314; TRP-1314; SER-1321; CYS-1339; HIS-1347; ASN-1361
RP AND THR-1424, AND VARIANTS ASP-61; ARG-207; GLY-265; GLU-281; VAL-319;
RP LYS-497; ALA-614; GLN-633; HIS-953; CYS-1241 AND GLN-1268.
RX MEDLINE=21426347; PubMed=11536079;
RA Le Saux O., Beck K., Sachsinger C., Silvestri C., Treiber C.,
Goering H.H.H., Johnson E.W., De Paep A., Pope P.M.,
Pasquali-Ronchetti I., Barcovich L., Terry S., Boyd C.D.;
RT "A spectrum of ABCG6 mutations is responsible for pseudoxanthoma
elasticum";
RL Am. J. Hum. Genet. 69:749-764(2001).
RN [12]
RP VARIANTS PXE 60-ARG--TYR-62 DEL; ARG-364 AND ARG-1354, AND VARIANT
RP GLY-265.
RX MEDLINE=21558431; PubMed=11702217; DOI=10.1007/s004390100592;
RA Puikinen L., Nakano A., Ringfeil F., Uitto J.;
RT "Identification of ABCG6 pseudogenes on human chromosome 16p:
implications for mutation detection in pseudoxanthoma elasticum";
RL Hum. Genet. 109:356-365(2001).
RN [13]
RP VARIANTS ALA-614; GLN-632 AND GLN-1268.
RX MEDLINE=21632106; PubMed=11776382;
RA Wang J., Near S., Young K., Connelly P.W., Hegele R.A.;
RT "ABCG6 gene polymorphism associated with variation in plasma
lipoproteins";
RL J. Hum. Genet. 46:699-705(2001).
CC -!- FUNCTION: May participate directly in the active transport of
drugs into subcellular organelles or influence drug distribution
indirectly. Transports glutathione conjugates as leukotriene-c4
(LUTC4) and N-ethylmaleimide S-glutathione (NEM-GS).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in kidney and liver. Very low
expression in other tissues.
CC -!- DISEASE: Defects in ABCG6 are a cause of autosomal dominant
pseudoxanthoma elasticum (AD-PXE) [MIM:177850]. PXE is a disorder
characterized by calcification of elastic fibers in skin, arteries
and retina that results in dermal lesions with associated laxity
and loss of elasticity, arterial insufficiency and retinal
hemorrhages leading to macular degeneration.
CC -!- DISEASE: Defects in ABCG6 are a cause of autosomal recessive
pseudoxanthoma elasticum (AR-PXE) [MIM:264800].
CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
gene model prediction.
CC -!- DATABASE: NAME=Mutations of the ABCG6 gene;
NOTE=Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/abcc6mut.htm".

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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC ENBL; AF076622; AAC79696.1; -;
DR ENBL; U91318; AAC15785.1; ALT_SEQ.
DR ENBL; AF168791; AAD51293.1; -;
DR HSSP; P08716; IMT0.
DR Genew; HGNC:57; ABCG6.
DR MIM; 603234; -;

DR MIM; 177850; -;
DR MIM; 264800; -;
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005886; F:ATP binding; TAS.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; TAS.
DR GO; GO:0005215; F:transporter activity; TAS.
DR GO; GO:0042493; P:response to drug; TAS.
DR GO; GO:0005810; P:transport; TAS.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR005292; MRP_assoc.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 2.
DR TIGRFAMs; TIGR00957; MRP_assoc_pro; 1.
DR PROSITE; PS00929; ABC_TMIF; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
DR ATP-binding; Disease mutation; Glycoprotein; Polymorphism; Repeat;
KW Transmembrane; Transport; Vision.
FT DOMAIN 1 31 Extracellular (By similarity).
FT TRANSMEM 32 52 1 (By similarity).
FT DOMAIN 53 72 Cytoplasmic (By similarity).
FT TRANSMEM 73 93 2 (By similarity).
FT DOMAIN 94 98 Extracellular (By similarity).
FT TRANSMEM 99 119 3 (By similarity).
FT DOMAIN 120 131 Cytoplasmic (By similarity).
FT TRANSMEM 132 149 4 (By similarity).
FT DOMAIN 150 167 Extracellular (By similarity).
FT TRANSMEM 168 188 5 (By similarity).
FT DOMAIN 189 302 Cytoplasmic (By similarity).
FT TRANSMEM 303 323 6 (By similarity).
FT DOMAIN 324 349 Extracellular (By similarity).
FT TRANSMEM 350 370 7 (By similarity).
FT DOMAIN 371 426 Cytoplasmic (By similarity).
FT TRANSMEM 427 447 8 (By similarity).
FT DOMAIN 448 450 Extracellular (By similarity).
FT TRANSMEM 451 471 9 (By similarity).
Query Match 77.8%; Score 42; DB 1; Length 1503;
Best Local Similarity 71.4%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWLTTW 7
Db 965 GYWLTLW 971
ID Q82Z85 PRELIMINARY; PRT; 266 AA.
AC Q82Z85;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
DE OrderedLocusNames=EF31185;
GN Enterococcus faecalis (Streptococcus faecalis).
OS Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,

| | | |
|--|--|---|
| DT | 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | |
| DE | Transport protein related protein. | |
| GN | OrderedLocusNames=Ta0692; | |
| GN | Thermoplasma acidophilum. | |
| OC | Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmatiales; | |
| OC | Thermoplasmatataceae; Thermoplasma. | |
| OC | NCBI_TaxID=2303; | |
| RP | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RC | STRAIN=DSM 1728; | |
| RC | MEDLINE=20479972; PubMed=11029001; | |
| RA | Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., | |
| RA | Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; | |
| RT | "The genome sequence of the thermoacidophilic scavenger Thermoplasma | |
| RT | acidophilum."; | |
| RL | Nature 407:508-513 (2000). | |
| DR | EMBL; AL445085; CAC11830.1; " | |
| DR | GO; GO:0016021; C:integral to membrane; IEA. | |
| DR | GO; GO:0005215; F:transporter activity; IEA. | |
| GO | GO; GO:0006810; P:transport; IEA. | |
| DR | InterPro; IPR007114; MFS. | |
| DR | PROSITE; PS50850; MFS; 1. | |
| KW | Complete proteome. | |
| SQ | SEQUENCE 413 AA; 45192 MW; 307093BC358063D4 CRC64; | |
| | | |
| QY | Query Match | 75.9%; Score 41; DB 2; Length 413; |
| DB | Best Local Similarity | 62.5%; Pred. No. 2.5e+02; |
| | Matches | 5; Conservative 2; Mismatches 1; Indels 0; Gaps |
| | | |
| QY | 1 GYWTIMG 8 | |
| DB | | |
| | 354 GFWETLWG 361 | |
| | | |
| RESULT 14 | | |
| Q97VB7 | | |
| ID | Q97VB7 PRELIMINARY; | PRT; 419 AA. |
| IC | Q97VB7; | |
| DT | 01-OCT-2001 (TrEMBLrel. 18, Created) | |
| DT | 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | |
| DE | Permease. | |
| GN | OrderedLocusNames=SSO2718; | |
| OS | Sulfolobus solfataricus. | |
| OC | Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; | |
| OC | Sulfolobus. | |
| OC | NCBI_TaxID=2287; | |
| RN | [1] | |
| RN | SEQUENCE FROM N.A. | |
| RC | STRAIN=ATCC 35092 / DSM 1617 / P2; | |
| RC | MEDLINE=21332296; PubMed=11427726; | |
| RA | She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., | |
| RA | Waynez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., | |
| RA | De Moors A., Erasuo G., Fletcher C., Gordon P.M.K., | |
| RA | Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X., | |
| RA | Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., | |
| RA | Charlebois R.L., Doolittle W.F., Duguet N., Gaasterland T., | |
| RA | Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.; | |
| RT | "The complete genome of the crenarchaeon Sulfolobus solfataricus P2. | |
| RT | proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001). | |
| EMBL; AE006865; AAK42828.1; " | | |
| PIR; E90446; E90446. | | |
| GO; GO:0016021; C:integral to membrane; IEA. | | |
| GO; GO:0005215; F:transporter activity; IEA. | | |
| GO; GO:0006810; P:transport; IEA. | | |
| InterPro; IPR007114; MFS. | | |
| InterPro; IPR005828; Sub transporter. | | |
| PFam; PF00083; Sugar tr; 1. | | |
| PROSITE; PS50850; MFS; 1. | | |
| KW | Complete proteome. | |
| SQ | SEQUENCE 419 AA; 46499 MW; 6DB6AB6B5C6DA267 CRC64; | |

Query Match 75.9%; Score 41; DB 2; Length 419;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYWLTIW 8
Db 365 GFWETLWG 372

RESULT 15

Q8DMV4 PRELIMINARY; PRT; 736 AA.
AC Q8DMV4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cellulose synthase.
GN OrderedLocustNames=tl0007;
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Kato H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR ENBL; AP005369; BAC07560.1; -.
DR InterPro; IPR001173; Glyco_trans 2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 736 AA; 85049 MW; D31C506166FD9624 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 736;
Best Local Similarity 85.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYWLTIW 7
Db 557 GYWLHIW 563

Search completed: January 3, 2005, 12:13:06
Job time : 190 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:13:55 ; Search time 148 Seconds
(without alignments)
19.391 Million cell updates/sec

Title: SEQ32

Perfect score: 54

Sequence: 1 gylwtwg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 153769

Minimum DB seq length: 0

Maximum-DB-seq-length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

- 1: Genesep1980s.*
- 2: Genesep1990s.*
- 3: Genesep2000s.*
- 4: Genesep2001s.*
- 5: Genesep2002s.*
- 6: Genesep2003as.*
- 7: Genesep2003bs.*
- 8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 33 | 61.1 | 7 | 5 | ABP53964 |
| 2 | 33 | 61.1 | 8 | 5 | ABP53965 |
| 3 | 32 | 59.3 | 7 | 3 | AAV76794 Somatosta |
| 4 | 32 | 59.3 | 7 | 5 | ABP53418 Backbone |
| 5 | 31 | 57.4 | 8 | 2 | AAW97529 Antigenic |
| 6 | 29 | 53.7 | 5 | 2 | AAW29452 Endotheli |
| 7 | 29 | 53.7 | 5 | 2 | AAW69224 Endotheli |
| 8 | 29 | 53.7 | 5 | 2 | AAW56531 Antigenic |
| 9 | 29 | 53.7 | 7 | 8 | ADJ25834 Tyrosine |
| 10 | 29 | 53.7 | 8 | 4 | ABP22594 HIV A11 m |
| 11 | 29 | 53.7 | 8 | 4 | ABP14287 HIV A03 s |
| 12 | 29 | 53.7 | 8 | 4 | ABP18686 HIV B62 s |
| 13 | 29 | 53.7 | 8 | 4 | ABP20292 HIV A03 m |
| 14 | 29 | 53.7 | 8 | 4 | ABP19992 HIV A03 m |
| 15 | 29 | 53.7 | 8 | 4 | ABP12050 HIV A02 s |
| 16 | 29 | 53.7 | 8 | 4 | ABP14288 HIV A03 s |
| 17 | 29 | 53.7 | 8 | 4 | ABP16999 HIV B27 s |
| 18 | 29 | 53.7 | 8 | 4 | ABP22402 HIV A11 m |
| 19 | 29 | 53.7 | 8 | 7 | ADL17320 DENGIN-18 |
| 20 | 29 | 53.7 | 8 | 8 | ADH62133 Cyclic an |
| 21 | 29 | 53.7 | 8 | 8 | ADH62029 Cyclic an |
| 22 | 29 | 53.7 | 8 | 8 | ADH62062 Cyclic an |
| 23 | 29 | 53.7 | 8 | 8 | ADP67844 Anti-micr |
| 24 | 29 | 53.7 | 8 | 8 | ADP67877 Anti-micr |
| 25 | 29 | 53.7 | 8 | 8 | ADP67948 Anti-micr |

| | | | | | | |
|----|----|------|---|---|----------|--------------------|
| 26 | 29 | 53.7 | 8 | 8 | ADQ28160 | Adq28160 Excluded |
| 27 | 29 | 53.7 | 8 | 8 | ADQ28097 | Adq28097 Excluded |
| 28 | 29 | 53.7 | 8 | 8 | ADQ28067 | Adq28067 Excluded |
| 29 | 28 | 51.9 | 6 | 2 | AAW20438 | AAW20438 Anti-b-en |
| 30 | 28 | 51.9 | 6 | 2 | AAW93713 | AAW93713 Cyclic an |
| 31 | 28 | 51.9 | 8 | 5 | ADH62036 | ADH62036 Cyclic an |
| 32 | 28 | 51.9 | 8 | 8 | ADH62037 | ADH62037 Cyclic an |
| 33 | 28 | 51.9 | 8 | 8 | ADH62043 | ADH62043 Cyclic an |
| 34 | 28 | 51.9 | 8 | 8 | ADH62038 | ADH62038 Cyclic an |
| 35 | 28 | 51.9 | 8 | 8 | ADH62065 | ADH62065 Cyclic an |
| 36 | 28 | 51.9 | 8 | 8 | ADP67852 | ADP67852 Anti-micr |
| 37 | 28 | 51.9 | 8 | 8 | ADP67858 | ADP67858 Anti-micr |
| 38 | 28 | 51.9 | 8 | 8 | ADP67880 | ADP67880 Anti-micr |
| 39 | 28 | 51.9 | 8 | 8 | ADP67853 | ADP67853 Anti-micr |
| 40 | 28 | 51.9 | 8 | 8 | ADP67851 | ADP67851 Anti-micr |
| 41 | 28 | 51.9 | 8 | 8 | ADQ28080 | ADQ28080 Excluded |
| 42 | 28 | 51.9 | 8 | 8 | ADQ28074 | ADQ28074 Excluded |
| 43 | 28 | 51.9 | 8 | 8 | ADQ28099 | ADQ28099 Excluded |
| 44 | 28 | 51.9 | 8 | 8 | ADQ28073 | ADQ28073 Excluded |
| 45 | 28 | 51.9 | 8 | 8 | ADQ28073 | ADQ28073 Excluded |

ALIGNMENTS

RESULT 1
ABP53964
ID ABP53964 standard; peptide; 7 AA.
XX ABP53964;
AC ABP53964;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:67.
XX

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
vulnerary; cell surface receptor; cancer; neovascularisation;
liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
diabetes; PDGF; platelet derived growth factor.
XX Homo sapiens.
OS
OS Synthetic.
FH
FH Key Location/Qualifiers
FT Misc-difference 4..6 /note= "X is any amino acid"

FT
FT WO200257299-A2.
XX
XX PN
XX PD
XX PF
XX PR
XX PA
XX FA
XX XX
XX PI
XX DR
XX XX
XX PT
XX PS
XX CC
XX CC

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
such as cancer and diseases of neovascularization.

Claim 21; Page 81; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and
inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
have cytostatic, hepatotropic, antiinflammatory, hypotensive,

CC antidiabetic and vulnary activities, and can be used in gene therapy.
 CC Compositions and methods from the present invention are useful for
 CC diagnosing, evaluating and treating disorders mediated by the activity of
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence
 CC represents a specifically claimed VEGFR-3 binding peptide from the
 CC present invention
 XX
 SQ Sequence 7 AA;

Query Match 61.1%; Score 33; DB 5; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
 ||||
 Db 1 GYWXXXW 7

RESULT 2
 ABP53965
 ID ABP53965 standard; peptide; 8 AA.

AC ABP53965;

XX 09-JAN-2003 (first entry)

XX VEGFR-3 binding peptide SEQ ID NO:68.

XX Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
 KW vulnary; cell surface receptor; cancer; neovascularisation;
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
 KW diabetes; PDGF; platelet derived growth factor.
 XX

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 4. .6 /note= "X is any amino acid"

FT Misc-difference 8 /note= "any amino acid"

FT WO200257299-A2.

XX 25-JUL-2002.

XX 16-JAN-2002; 2002WO-IB000099.

XX 17-JAN-2001; 2001US-0262476P.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (LICN) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;

XX WPI; 2002-691521/74.

XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
 PT such as cancer and diseases of neovascularization.
 XX

PS Claim 22; Page 81; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
 CC

CC antidiabetic and vulnary activities, and can be used in gene therapy.
 CC Compositions and methods from the present invention are useful for
 CC diagnosing, evaluating and treating disorders mediated by the activity of
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence
 CC represents a specifically claimed VEGFR-3 binding peptide from the
 CC present invention
 XX
 SQ Sequence 8 AA;

Query Match 61.1%; Score 33; DB 5; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
 ||||
 Db 1 GYWXXXW 7

RESULT 3
 AAY76794
 ID AAY76794 standard; peptide; 7 AA.

AC AAY76794;

XX 20-APR-2000 (first entry)

XX Somatostatin analogue peptide 3181.

XX Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;
 KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;
 KW gastrointestinal disorder; inflammatory disease; pancreatitis;
 KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;
 KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;
 KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
 XX

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 3 /note= "D-form residue"

FT Modified-site 7 /note= "Trp-NH2"

XX WO9965508-A1.

XX 23-DEC-1999.

XX 15-JUN-1999; 99WO-IL000329.

XX 19-JUN-1998; 98US-00100360.

XX 02-DEC-1998; 98US-00203389.

XX (PEPT-) PEPTOR LTD.

XX Hornik V, Afargan MM, Gellerman G;

XX WPI; 2000-136888/12.

XX Cyclized somatostatin analogs for inhibiting growth hormone secretion
 PT from anterior pituitary and as antiproliferative agents for the treatment
 PT of tumors.
 XX

PS Example 11; Page 61; 82pp; English.

XX This sequence represents a somatostatin analogue of the invention. The
 CC invention relates to a backbone cyclised somatostatin analogue that has
 CC one building unit containing a nitrogen atom of the peptide backbone
 CC connected to a bridging group comprising an amide, thioether, thioester

or disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders such as cancers, autoimmune diseases, endocrine disorders, diabetic-associated complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-surgical pain. It may also be used for diagnosing cancer. The backbone cyclic analogue is used for imaging the existence of metastases. Somatostatin and hormone-dependent tumours. They reduce diarrhoea through the inhibition of vasoactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type 2 and 5 receptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe

XX Sequence 7 AA;

Query Match 59.3%; Score 32; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GYWLTIW 7
Db 1 GYWKVCW 7

RESULT 4

ABP53418
ID ABP53418 standard; peptide; 7 AA.

XX AC ABP53418;

XX DT 19-NOV-2002 (first entry)

XX DE Backbone cyclised somatostatin analogue PTR 3181.

XX KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatostatin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antiinflammatory; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis; pancreatitis; post-surgical pain.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminally modified with Fmoc (fluorenylmethoxycarbonyl)"
FT Misc-difference 3
FT Modified-site 7 /note= "D form residue"
FT Modified-site 7 /note= "amidated"

XX PN US2002052315-A1.

XX PD 02-MAY-2002.

XX PF 13-DEC-2000; 2000US-00734583.

XX PR 19-JUN-1998; 98US-00100360.

XX PR 02-DEC-1998; 98US-00203389.

XX PR 15-JUN-1999; 99WO-IL000329.

XX PA (HORN/) HORNIK V.

XX PA (AFAR/) AFARGAN M M.

XX PA (GSELL/) GELLERMAN G.

XX PI Hornik V, Afargan MM, Gellerman G;

XX DR WPI; 2002-681319/73.

XX PT New backbone cyclised somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.

XX PS Example 12; Page 21; 30pp; English.

XX CC The present invention describes backbone cyclised somatostatin analogues (I) that incorporates at least one building unit containing one nitrogen atom of the peptide backbone connected to a bridging group (comprising an amide, thioether, thioester or disulfide) where at least one building unit is connected via the bridging group to form a cyclic structure with a moiety selected from the group consisting of a second building unit, the side chain of an amino acid residue of the sequence or the N-terminal amino acid residue. (I) has antiarteriosclerotic, immunosuppressive, cytostatic, antidiabetic, antiinflammatory and analgesic activities, and can be used as a somatostatin receptor ligand. (I) are useful in the treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-associated complications, endocrine disorders, inflammation, gastrointestinal disorders, pancreatitis, post-surgical pain, and restenosis. (I) can also be used in the diagnosis of cancer, by imaging the existence of metastases, it being labeled with a detectable probe. The present sequence represents a backbone cyclised somatostatin analogue from the present invention

XX SQ Sequence 7 AA;

Query Match 59.3%; Score 32; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7

Db 1 GYWKVCW 7

RESULT 5

AAW97529
ID AAW97529 standard; peptide; 8 AA.

XX AC AAW97529;

XX DT 19-MAY-1999 (first entry)

XX DE Antigenic site of HN protein loop beta-4L23.

XX KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae; virus epitope; attachment protein; vaccine; immunodominant epitope.

XX OS Measles virus.

XX PN WO9902695-A2.

XX PD 21-JAN-1999.

XX PF 08-JUL-1998; 98WO-NL000390.

XX PR 08-JUL-1997; 97EP-00202100.

XX PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

XX PI Langedijk JPM, Van Oirschot JT;

XX DR WPI; 1999-120896/10.

XX PT Isolated proteinaceous substance - comprising at least one virus epitope derived from an attachment protein of a paramyxovirus.

XX PS Disclosure; Page 48; 63pp; English.

XX CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-neuraminidase (HN) protein of the paramyxoviridae. The specification

CC describes 3-D models identifying a proteinaceous substance comprising at least one virus epitope derived from the attachment protein, which corresponds to an antigenic site present on one of the loops of HN. The antigenic sites can be used to produce vaccines, to detect the viruses, and to select the immunodominant epitope

XX
SQ Sequence 8 AA;

Query Match 57.4%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWLTII 6
|||||
Db 4 YWLTII 8

RESULT 6
AAR29452
ID AAR29452 standard; peptide; 5 AA.

XX AC AAR29452;

XX 25-MAR-2003 (revised)
DT 13-APR-1993 (first entry)

XX Endothelin antagonist peptide.

XX Hypertension; myocardial infarction; congestive heart failure;
KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW acute renal failure; preeclampsia; diabetes; metabolic; endocrinological;
KW neurological; disorders.

XX Synthetic.

Key Location/Qualifiers
FT Modified-site 1 /note= "Ac-D-Trp"

XX WO9220706-A1.

XX 26-NOV-1992.

XX 24-APR-1992; 92WO-US003408.

XX 16-MAY-1991; 91US-00701274.

XX 18-DEC-1991; 91US-00809746.

XX (WARN) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, Taylor MD;

XX WPI; 1992-415706/50.

XX New peptide(s) used as endothelin antagonists - for treating hypertension, metabolic and endocrine disorders, heart failure, diabetes, asthma, neurological disorders, etc.

XX Claim 5; Page 95; 116pp; English.

XX The peptide is an endothelin antagonist useful in controlling hypertension, myocardial infarction, congestive heart failure, endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias, acute renal failure, preeclampsia, diabetes and metabolic, endocrinological and neurological disorders. Administration is oral parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/ day. It may be prepared by conventional peptide synthesis. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 5 AA;

Query Match 53.7%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 WLTII 7
|||
Db 1 WLDII 5

RESULT 7

AAR69224
ID AAR69224 standard; peptide; 5 AA.

XX AC AAR69224;

XX 25-MAR-2003 (revised)
DT 06-MAR-1995 (first entry)

XX Endothelin C-terminal peptide analog, useful as antagonist.

XX Endothelin; ET-1; receptor; antagonist.

XX Synthetic.

Key Location/Qualifiers
FT Misc-difference 1 /note= "Ac-D-Trp"

XX WO9414843-A1.

XX 07-JUL-1994.

XX 17-DEC-1993; 93WO-US012377.

XX 21-DEC-1992; 92US-00995480.

XX (WARN) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, He JX, Taylor MD;

XX WPI; 1994-234617/28.

XX New hexa-peptide derivs. inhibiting endothelin - for treatment of e.g. renal failure, hypertension, asthma, restenosis, angina, cancer etc.

XX Claim 5; Page 119; 146pp; English.

XX Novel antagonists of endothelin are claimed which are C-terminal hexapeptides and analogs of ET-1. The first (N-terminal) amino acid of the new peptides has D-configuration. The peptides are claimed generically. The present peptide is a specifically claimed example of the generic compounds. The peptides are useful for treating hypertension, metabolic and endocrine disorders, congestive heart failure, myocardial infarction, endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute and chronic renal failure, preeclampsia, diabetes, neurological disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel disease, gastric mucosal damage, Raynaud's disease, restenosis, percutaneous transluminal coronary angioplasty, angina and cancer. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 5 AA;

Query Match 53.7%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTII 7
|||
Db 1 WLDII 5

RESULT 8

AAW56531
ID AAW56531 standard; peptide; 5 AA.

XX

AC AAW56531;
 XX
 DT 06-AUG-1998 (first entry)
 XX
 DE Antigenic HIV-1 peptide used in diagnostic test device of invention.
 XX
 KW HIV-1; antigen; test device; detection; HIV infection; antibody;
 KW whole blood; hormone; vitamin; microbial pathogen; drug.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 FN WO9813519-A1.
 XX
 XX 02-APR-1998.
 XX
 PD 25-SEP-1997; 97WO-US017129.
 XX
 PF 25-SEP-1996; 96US-0026681P.
 XX
 PR 18-AUG-1997; 97US-00912580.
 XX
 XX (UVHE-) UNIVERSAL HEALTHWATCH INC.
 XX
 XX Childs MA, Bernstein D;
 XX
 XX WPI; 1998-230723/20.
 XX
 XX Diagnostic test device - provides homogeneous fluid flow and increased
 PT chemical resistance, especially for detecting antibodies to human
 PT immunodeficiency virus.
 XX
 XX Claim 39; Page 36; 50pp; English.
 XX
 XX AAW56525-36 represent antigenic Human immunodeficiency virus type 1 (HIV-
 CC 1) peptides used in the test device of the invention. This test device
 CC comprises, in a housing, an absorbent pad, a reagent layer containing
 CC immobilised test antigens and a filter. The housing has an opening,
 CC adjacent to the filter, for applying an aqueous sample, and the filter is
 CC held in contact with the reagent layer by a sleeve. The filter protrudes
 CC from the sleeve such that it exerts a greater pressure on the reagent
 CC layer than does the sleeve. The device is specifically used to detect HIV
 CC infection from presence of specific antibodies in whole blood, but many
 CC other analytes can also be detected, e.g. amino acids, nucleic acid,
 CC hormones, vitamins, microbial pathogens and drugs (therapeutic or
 CC illicit)
 XX
 SQ Sequence 5 AA;
 Query Match 53.7%; Score 29; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LTVWG 8
 DB 1 LTVWG 5
 RESULT 9
 ADJ25834
 ID ADJ25834 standard; peptide; 7 AA.
 XX
 XX ADJ25834;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 DE Tyrosine tRNA synthetase binding peptide group 2 motif.
 XX
 KW ligand identification; peptide library;
 KW complementary combinatorial library; tyrosine tRNA synthetase.
 XX
 OS Synthetic.
 XX
 XX US6617114-B1.
 FN

XX 09-SEP-2003.
 PD
 XX 30-APR-1998; 98US-00069827.
 PF
 XX 31-OCT-1996; 96US-00740671.
 PR 31-OCT-1997; 97WO-US019638.
 PR 31-MAR-1998; 98US-00050359.
 XX
 XX (KARO-) KARO BIO AB.
 PA
 XX Fowlkes DM, Kay BK, Frelinger JA, Hyde-Deruysscher RP;
 FI WPI; 2004-068186/07.
 XX
 DR Identification of ligand that can mediate biological activity of target
 XX protein, comprises screening first combinatorial library having first
 PT member ligands for binding to target protein to identify target-binding
 PT ligand(s).
 XX
 PS Example 5; SEQ ID NO 94; 98pp; English.
 XX
 XX The invention relates to a method of identifying a ligand that can
 CC mediate the biological activity of target protein via inhibition of the
 CC binding of target protein to a binding partner ligand comprising
 CC screening first combinatorial library having first member ligands for
 CC binding to target protein to identify target-binding ligand(s). The
 CC method is useful for identifying ligands that can mediate the biological
 CC activity of target proteins via inhibition of the binding of target that
 CC protein to a binding partner ligand. The invention does not require that
 CC the natural binding partner be used as reagent. The need for the natural
 CC binding partner is obviated with the use of complementary combinatorial
 CC libraries. The present sequence is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 53.7%; Score 29; DB 8; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 YWLTWG 8
 DB 1 YWVPDWG 7
 RESULT 10
 ABP22594
 ID ABP22594 standard; peptide; 8 AA.
 XX
 XX AC ABP22594;
 XX
 XX 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 XX HIV A11 motif env peptide #317.
 DE
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX WO200124810-A1.
 FN
 XX 12-APR-2001.
 PD
 XX 05-OCT-2000; 2000WO-US027766.
 XX
 XX 05-OCT-1999; 99US-00412863.
 PR
 XX (EPIM-) EPIMMUNE INC.
 XX
 XX

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PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX Claim 32; Page 332; 448pp; English.
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
XX be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines. An
XX additional advantage of an group-based vaccine approach is the ability to
XX combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.. (Updated on 11-SEP-2003 to standardise OS field)
XX Sequence 8 AA;
SQ Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIWG 8
DB 2 LTVWG 6

RESULT 11
ABP14287
ID ABP14287 standard; peptide; 8 AA.
XX AC ABP14287;
XX DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX HIV A03 super motif env peptide #27.
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
XX vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX vaccine; HIV infection; immunisation; virucide.
XX Human immunodeficiency virus 1.
XX WO200124810-A1.
XX 12-APR-2001.
XX 05-OCT-2000; 2000WO-US027766.
XX 05-OCT-1999; 99US-00412863.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.

XX DR
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX Claim 32; Page 161; 448pp; English.
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
XX be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines. An
XX additional advantage of an group-based vaccine approach is the ability to
XX combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.. (Updated on 11-SEP-2003 to standardise OS field)
XX Sequence 8 AA;
SQ Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIWG 8
DB 2 LTVWG 6

RESULT 12
ABP18686
ID ABP18686 standard; peptide; 8 AA.
XX AC ABP18686;
XX DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX HIV B62 super motif env peptide #261.
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
XX vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX vaccine; HIV infection; immunisation; virucide.
XX Human immunodeficiency virus 1.
XX WO200124810-A1.
XX 12-APR-2001.
XX 05-OCT-2000; 2000WO-US027766.
XX 05-OCT-1999; 99US-00412863.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.

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XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS
XX
XX Claim 32; Page 252; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABP25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 8 AA;
SQ

Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTIWG 8
||:|
Db 3 LTVWG 7

RESULT 13
ABP20292
ID ABP20292 standard; peptide; 8 AA.
XX
XX AC ABP20292;
XX
XX DT 11-SEP-2003 (revised)
XX DT 15-JUL-2002 (first entry)
XX
XX DE HIV A03 motif env peptide #496.
XX
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
XX KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX KW vaccine; HIV infection; immunisation; virucide.
XX
XX OS Human immunodeficiency virus 1.
XX OS
XX PN WO200124810-A1.
XX
XX PD 12-APR-2001.
XX
XX PF 05-OCT-2000; 2000WO-US027766.
XX
XX PR 05-OCT-1999; 99US-00412863.
XX
XX PA (EPIM-) EPIMMUNE INC.
XX
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX DR WPI; 2001-354887/37.
XX
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.

PT peptide groups, useful for vaccinating against HIV-1.
XX
XX PS
XX
XX Claim 32; Page 285; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABP25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 8 AA;
SQ

Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTIWG 8
||:|
Db 2 LTVWG 6

RESULT 14
ABP19992
ID ABP19992 standard; peptide; 8 AA.
XX
XX AC ABP19992;
XX
XX DT 11-SEP-2003 (revised)
XX DT 15-JUL-2002 (first entry)
XX
XX DE HIV A03 motif env peptide #196.
XX
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
XX KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX KW vaccine; HIV infection; immunisation; virucide.
XX
XX OS Human immunodeficiency virus 1.
XX OS
XX PN WO200124810-A1.
XX
XX PD 12-APR-2001.
XX
XX PF 05-OCT-2000; 2000WO-US027766.
XX
XX PR 05-OCT-1999; 99US-00412863.
XX
XX PA (EPIM-) EPIMMUNE INC.
XX
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX DR WPI; 2001-354887/37.
XX
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.

```

PS Claim 32; Page 279; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;
Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 LTIWG 8
DB 2 LTVWG 6

RESULT 15
ABP12050
ID ABP12050 standard; peptide; 8 AA.
XX
AC ABP12050;
XX
XX
XX 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif env peptide #107.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US027766.
XX
XX 05-OCT-1999; 99US-00412863.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32; Page 116; 448pp; English.
XX

```

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

Search completed: January 3, 2005, 12:27:56
Job time : 150 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:23:00 ; Search time 37 Seconds
(without alignments)
14.339 Million cell updates/sec

Title: SEQ32

Perfect score: 54

Sequence: 1 gywltwg 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 73656

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 29 | 53.7 | 7 | 4 | US-09-069-827A-94 |
| 2 | 28 | 51.9 | 8 | 3 | US-09-315-304B-1649 |
| 3 | 27.5 | 50.9 | 6 | 1 | US-08-191-571-12 |
| 4 | 27.5 | 50.9 | 6 | 5 | PCT-US95-00296-12 |
| 5 | 27 | 50.0 | 8 | 3 | US-08-586-670A-17 |
| 6 | 27 | 50.0 | 8 | 3 | US-09-082-279B-1495 |
| 7 | 27 | 50.0 | 8 | 4 | US-08-834-784-1495 |
| 8 | 27 | 50.0 | 8 | 4 | US-09-350-641C-1650 |
| 9 | 26 | 48.1 | 5 | 1 | US-08-353-400-27 |
| 10 | 26 | 48.1 | 6 | 1 | US-08-415-099A-3 |
| 11 | 26 | 48.1 | 8 | 1 | US-08-415-099A-4 |
| 12 | 26 | 48.1 | 8 | 3 | US-08-467-472C-5 |
| 13 | 26 | 48.1 | 8 | 3 | US-08-467-472C-6 |
| 14 | 26 | 48.1 | 8 | 3 | US-09-082-279B-1500 |
| 15 | 26 | 48.1 | 8 | 3 | US-09-384-061-5 |
| 16 | 26 | 48.1 | 8 | 3 | US-09-384-061-6 |
| 17 | 26 | 48.1 | 8 | 4 | US-09-834-784-1500 |
| 18 | 26 | 48.1 | 8 | 4 | US-08-632-444B-9 |
| 19 | 26 | 48.1 | 8 | 4 | US-09-350-641C-1655 |
| 20 | 26 | 48.1 | 8 | 4 | US-09-852-870A-5 |
| 21 | 25.5 | 47.2 | 8 | 1 | US-08-191-571-21 |
| 22 | 25.5 | 47.2 | 8 | 5 | PCT-US95-00296-21 |
| 23 | 25 | 46.3 | 5 | 4 | US-09-155-106-1 |
| 24 | 25 | 46.3 | 6 | 2 | US-08-660-747-56 |
| 25 | 25 | 46.3 | 8 | 4 | US-09-125-641-1 |
| 26 | 25 | 46.3 | 8 | 4 | US-09-125-641-2 |
| 27 | 24.5 | 45.4 | 8 | 3 | US-08-481-968A-19 |

| | | | | | |
|----|------|------|---|---|---------------------|
| 28 | 24.5 | 45.4 | 8 | 3 | US-08-154-712B-19 |
| 29 | 24.5 | 45.4 | 8 | 4 | US-09-947-925A-19 |
| 30 | 24 | 44.4 | 5 | 4 | US-08-753-750B-38 |
| 31 | 24 | 44.4 | 5 | 6 | 5185431-15 |
| 32 | 24 | 44.4 | 6 | 1 | US-07-718-577-6 |
| 33 | 24 | 44.4 | 6 | 2 | US-08-660-747-60 |
| 34 | 24 | 44.4 | 7 | 3 | US-09-082-279B-653 |
| 35 | 24 | 44.4 | 7 | 3 | US-09-315-304B-653 |
| 36 | 24 | 44.4 | 7 | 3 | US-09-315-304B-1579 |
| 37 | 24 | 44.4 | 7 | 4 | US-09-388-788-2 |
| 38 | 24 | 44.4 | 7 | 4 | US-09-350-325-39 |
| 39 | 24 | 44.4 | 7 | 4 | US-09-834-784-653 |
| 40 | 24 | 44.4 | 7 | 4 | US-09-515-965A-653 |
| 41 | 24 | 44.4 | 7 | 4 | US-09-350-641C-653 |
| 42 | 24 | 44.4 | 7 | 4 | US-09-350-641C-1579 |
| 43 | 24 | 44.4 | 7 | 4 | US-09-563-222C-53 |
| 44 | 24 | 44.4 | 7 | 4 | US-09-350-841A-653 |
| 45 | 24 | 44.4 | 8 | 1 | US-08-073-028-47 |

ALIGNMENTS

RESULT 1

US-09-069-827A-94

; Sequence 94, Application US/09069827A

; Patent No. 6617114

; GENERAL INFORMATION:

APPLICANT: FOWLKES, Dana M

KAY, Brian K

FRELINGER, Jeffrey A

HYDE-DERUYSCHEER, Robin P

TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING

COMPLEMENTARY COMBINATORIAL LIBRARIES

NUMBER OF SEQUENCES: 178

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

STREET: 624 Ninth Street N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069, 827A

FILING DATE: 30-Apr-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/050,359

FILING DATE: 31-MAR-1998

APPLICATION NUMBER: PCT/US97/19638

FILING DATE: 31-OCT-1997

APPLICATION NUMBER: US 08/740,671

FILING DATE: 31-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: FOWLKES=4C

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 94:

US-09-069-827A-94

Query Match 53.7%; Score 29; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWLTWIG 8
||| |||
Db 1 YWPDWG 7

RESULT 2

US-09-315-304B-1649
; Sequence 1649, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1649
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-09-315-304B-1649

Query Match 51.9%; Score 28; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLTIWG 8
|:|:|
Db 1 WNSLWG 6

RESULT 3

US-08-191-571-12
; Sequence 12, Application US/08191571
; Patent No. 5521156
; GENERAL INFORMATION:
; APPLICANT: Owen, Thomas J.
; APPLICANT: Kudlacz, Elizabeth M
; APPLICANT: Buck, Stephen H
; APPLICANT: Harbeson, Scott L
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: P. O. Box 156300 2110 E. Galbraith Rd.
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: United States
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/191,571
; APPLICATION NUMBER: US/08/191,571
; FILING DATE: 03-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01718
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-948-6566
; TELEFAX: 513-948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-191-571-12

Query Match 50.9%; Score 27.5; DB 1; Length 6;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YWLTWIG 8
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Db 1 YWLR-WG 6

RESULT 4

PCT-US95-00296-12
; Sequence 12, Application PC/TUS9500296
; GENERAL INFORMATION:
; APPLICANT: Merrell Dow Pharmaceuticals Inc.
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: 2110 East Galbraith Road, P.O. Box 156300
; CITY: Cincinnati
; STATE: OH
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00296
; FILING DATE:

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01718A WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-948-6566
; TELEFAX: 513-948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
PCT-US95-00296-12

Query Match 50.9%; Score 27.5; DB 5; Length 6;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YWLTWIG 8
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Db 1 YWLR-WG 6

RESULT 5

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US-08-586-670A-17
; Sequence 17, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586.670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
; OTHER INFORMATION: is L-4-chlorophenylalanine; the Trp is in the
; OTHER INFORMATION: D conformation;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
; OTHER INFORMATION: is L-4-chlorophenylalanine; the Trp is in the
; OTHER INFORMATION: D conformation;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7..8
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The carboxyl group of the C-terminal
; OTHER INFORMATION: Thr is reduced to an alcohol;
;
US-08-586-670A-17
Query Match 50.0%; Score 27; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWL 5
Db 2 GYWK 6

RESULT 6
US-08-082-279B-1495
; Sequence 1495, Application US/09082279B
; Patent No. 6258782

```

```

; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1495
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-09-082-279B-1495
Query Match 50.0%; Score 27; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTIWG 8
Db 1 WDSLWG 6

RESULT 7
US-09-834-784-1495
; Sequence 1495, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1495
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-09-834-784-1495
Query Match 50.0%; Score 27; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTIWG 8
Db 1 WDSLWG 6

RESULT 8
US-09-350-641C-1650
; Sequence 1650, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

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; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1650
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
; US-09-350-641C-1650

Query Match 50.0%; Score 27; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTIW 8
| :|||
Db 1 WDSLWG 6

RESULT 9
US-08-353-400-27
; Sequence 27, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-27

Query Match 48.1%; Score 26; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWL 4
| :|||
Db 1 GYWI 4

RESULT 10
US-08-415-099A-3
; Sequence 3, Application US/08415099A
; Patent No. 5789384
; GENERAL INFORMATION:
; APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.
; TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Ther
```

```
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cytoven
; STREET: 10230 N.E. Points Drive, Suite 530
; CITY: Kirkland
; STATE: Washington
; COUNTRY: USA
; ZIP: 98033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.25 inch, 1.44Mb storage
; COMPUTER: IBM PC/486 Compatible
; OPERATING SYSTEM: MS-DOS 5.01
; SOFTWARE: Word for Windows 6.0-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,099A
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,386
; FILING DATE: 06-JUL-1994
; APPLICATION NUMBER: 08/026,341
; FILING DATE: March 4, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sundemo, John, S.
; REGISTRATION NUMBER: 34,446
; REFERENCE/DOCKET NUMBER: 15548-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-889-5804 (direct)
; TELEFAX: 1-206-822-3644
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; US-08-415-099A-3

Query Match 48.1%; Score 26; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTIW 7
| :|||
Db 2 WIWIW 6

RESULT 11
US-08-415-099A-4
; Sequence 4, Application US/08415099A
; Patent No. 5789384
; GENERAL INFORMATION:
; APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.
; TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Ther
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cytoven
; STREET: 10230 N.E. Points Drive, Suite 530
; CITY: Kirkland
; STATE: Washington
; COUNTRY: USA
; ZIP: 98033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.25 inch, 1.44Mb storage
; COMPUTER: IBM PC/486 Compatible
; OPERATING SYSTEM: MS-DOS 5.01
; SOFTWARE: Word for Windows 6.0-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,099A
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/271,386
FILING DATE: 06-JUL-1994
APPLICATION NUMBER: 08/026,341
FILING DATE: March 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Sundemo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 15548-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-889-5804(direct)
TELEFAX: 1-206-822-3644
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
US-08-415-099A-4

Query Match 48.1%; Score 26; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTW 7
| : | |
Db 2 WWTW 6

RESULT 12

US-08-467-472C-5
Sequence 5, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:

DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
FEATURE:
POSITION IN GENOME: N/A
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEN MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-5

Query Match 48.1%; Score 26; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 WLTW 7
| : | |
Db 3 FWKTSW 8

RESULT 13
US-08-467-472C-6
; Sequence 6, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE: 865 - 869
; PAGES: 1990
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:

; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
; US-08-467-472C-6

Query Match 48.1%; Score 26; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YMLTIW 7
Db 3 FWKTSW 8

RESULT 14
US-09-082-279B-1500
; Sequence 1500, Application US/09082279B
; Patent No. 6256782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1500
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
; US-09-082-279B-1500

Query Match 48.1%; Score 26; DB 3; Length 8;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTIW 7
Db 1 WASIW 5

RESULT 15
US-09-384-061-5
Sequence 5, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HADT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:

FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK P.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: BY
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-5
Query Match 48.1%; Score 26; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 YWLTW 7
Db 3 FWKTSW 8
Search completed: January 3, 2005, 12:32:37
Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:31:17 ; Search time 140 Seconds
(without alignments)
20.556 Million cell updates/sec

Title: SEQ32

Perfect score: 54

Sequence: 1 gywltiwg 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 83711

Minimum DB seq length: 0

Maximum-DB-seq-length: 8

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 33 | 61.1 | 7 | 13 | US-10-046-922-67 |
| 2 | 33 | 61.1 | 8 | 13 | US-10-046-922-68 |
| 3 | 27 | 50.0 | 8 | 14 | US-10-351-641-1650 |
| 4 | 26 | 48.1 | 7 | 9 | US-09-884-767A-38 |
| 5 | 26 | 48.1 | 7 | 16 | US-10-433-452A-3 |
| 6 | 26 | 48.1 | 8 | 9 | US-09-852-870A-5 |
| 7 | 26 | 48.1 | 8 | 14 | US-10-351-641-1655 |
| 8 | 26 | 48.1 | 8 | 15 | US-10-196-937A-9 |
| 9 | 26 | 48.1 | 8 | 16 | US-10-457-780-38 |
| 10 | 25.5 | 47.2 | 8 | 15 | US-10-367-580-227 |
| 11 | 25.5 | 47.2 | 8 | 15 | US-10-367-593-227 |
| 12 | 25.5 | 47.2 | 8 | 15 | US-10-367-594-227 |
| 13 | 25.5 | 47.2 | 8 | 15 | US-10-367-654-227 |

| | | | | | | |
|----|------|------|---|----|--------------------|--------------------|
| 14 | 25.5 | 47.2 | 8 | 15 | US-10-367-658-227 | Sequence 227, App |
| 15 | 25.5 | 47.2 | 8 | 15 | US-10-367-668-227 | Sequence 227, App |
| 16 | 25.5 | 47.2 | 8 | 16 | US-10-367-674-227 | Sequence 227, App |
| 17 | 25 | 46.3 | 5 | 10 | US-09-155-106-1 | Sequence 1, Appli |
| 18 | 25 | 46.3 | 7 | 14 | US-10-190-082-65 | Sequence 65, Appli |
| 19 | 25 | 46.3 | 7 | 14 | US-10-190-082-487 | Sequence 487, App |
| 20 | 25 | 46.3 | 7 | 17 | US-10-858-271-10 | Sequence 10, Appl |
| 21 | 25 | 46.3 | 8 | 14 | US-10-190-082-489 | Sequence 489, App |
| 22 | 25 | 46.3 | 8 | 14 | US-10-050-902-179 | Sequence 179, App |
| 23 | 25 | 46.3 | 8 | 14 | US-10-050-902-180 | Sequence 180, App |
| 24 | 25 | 46.3 | 8 | 14 | US-10-050-898-179 | Sequence 179, App |
| 25 | 25 | 46.3 | 8 | 14 | US-10-050-898-180 | Sequence 180, App |
| 26 | 25 | 46.3 | 8 | 14 | US-10-082-014-279 | Sequence 279, App |
| 27 | 25 | 46.3 | 8 | 14 | US-10-372-076-133 | Sequence 133, App |
| 28 | 25 | 46.3 | 8 | 15 | US-10-149-138-35 | Sequence 35, Appli |
| 29 | 25 | 46.3 | 8 | 15 | US-10-149-138-1999 | Sequence 1999, Ap |
| 30 | 25 | 46.3 | 8 | 15 | US-10-617-876-31 | Sequence 31, Appl |
| 31 | 25 | 46.3 | 8 | 15 | US-10-617-876-32 | Sequence 32, Appl |
| 32 | 25 | 46.3 | 8 | 16 | US-10-149-138-35 | Sequence 35, Appl |
| 33 | 25 | 46.3 | 8 | 16 | US-10-149-138-1999 | Sequence 1999, Ap |
| 34 | 25 | 46.3 | 8 | 16 | US-10-677-074-133 | Sequence 133, App |
| 35 | 24.5 | 45.4 | 6 | 17 | US-10-477-307-5 | Sequence 5, Appli |
| 36 | 24.5 | 45.4 | 8 | 9 | US-09-947-925A-19 | Sequence 19, Appl |
| 37 | 24 | 44.4 | 4 | 16 | US-10-386-575-12 | Sequence 12, Appl |
| 38 | 24 | 44.4 | 5 | 15 | US-10-436-549-496 | Sequence 496, App |
| 39 | 24 | 44.4 | 5 | 15 | US-10-436-549-525 | Sequence 525, App |
| 40 | 24 | 44.4 | 5 | 16 | US-10-712-425-496 | Sequence 496, App |
| 41 | 24 | 44.4 | 5 | 16 | US-10-712-425-525 | Sequence 525, App |
| 42 | 24 | 44.4 | 6 | 14 | US-10-414-524-34 | Sequence 34, Appl |
| 43 | 24 | 44.4 | 6 | 14 | US-10-407-079-65 | Sequence 65, Appl |
| 44 | 24 | 44.4 | 6 | 16 | US-10-346-737A-45 | Sequence 45, Appl |
| 45 | 24 | 44.4 | 7 | 10 | US-09-563-222-53 | Sequence 53, Appl |

ALIGNMENTS

RESULT 1

US-10-046-922-67
; Sequence 67, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivu, Hajime
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)...(6)
; OTHER INFORMATION: X at position 4-6 is any amino acid
US-10-046-922-67

Query Match 61.1%; Score 33; DB 13; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7

Db 1 GYWXW 7

RESULT 2

US-10-046-922-68
; Sequence 68, Application US/10046922

; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Eekki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 8
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (8)..(8)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-68

Query Match 61.1%; Score 33; DB 13; Length 8;
Best Local Similarity 57.4%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
| | | |
Db 1 GYWXW 7

RESULT 3
US-10-351-641-1650
; Sequence 1650, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1650
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-10-351-641-1650

Query Match 50.0%; Score 27; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLTIWG 8
| | | |
Db 1 WDSLWG 6

RESULT 4
US-09-884-767A-38

; Sequence 38, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-38

Query Match 48.1%; Score 26; DB 9; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWL 4
| | |
Db 1 GYWI 4

RESULT 5
US-10-433-452A-3
; Sequence 3, Application US/10433452A
; Publication No. US20040101905A1
; GENERAL INFORMATION:
; APPLICANT: Brekke, Ole Henrik
; APPLICANT: Lauvrak, Vigdis
; APPLICANT: Sandlie, Inger
; TITLE OF INVENTION: Hybrid Antibodies
; FILE REFERENCE: DEH-0014
; CURRENT APPLICATION NUMBER: US/10/433,452A
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: GB 0029407.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fc effector peptide
; NAME/KEY: VARIANT
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is R or a large hydrophobic amino acid, e.g. phenylalanine: W
; OTHER INFORMATION: F, tyrosine: Y, or tryptophan: W
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3)..(5)
; OTHER INFORMATION: Xaa is a less conserved or variable amino acid
US-10-433-452A-3

Query Match 48.1%; Score 26; DB 16; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 WLTIWG 8
| | | |
Db 2 WXXXWG 7

```
RESULT 6
US-09-852-870A-5
; Sequence 5, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-5
Query Match 48.1%; Score 26; DB 9; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 YWLTIW 7
Db 3 FWKTSW 8
RESULT 7
US-10-351-641-1655
; Sequence 1655, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1655
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-10-351-641-1655
Query Match 48.1%; Score 26; DB 14; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 WLTIW 7
Db 1 WASIW 5
RESULT 8
US-10-196-937A-9
; Sequence 9, Application US/10196937A
; Publication No. US20040024176A1
; GENERAL INFORMATION:
; APPLICANT: Ghadiri, Reza M.
; TITLE OF INVENTION: Cyclic Peptide Tube
; FILE REFERENCE: 397.2 Div 1/SCR 2381
; CURRENT APPLICATION NUMBER: US/10/196,937A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 08/632,444
; PRIOR FILING DATE: 1996-04-15
; PRIOR APPLICATION NUMBER: 08/320,922
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: 08/138,502
; PRIOR FILING DATE: 1993-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Length: 8 amino acids
; OTHER INFORMATION: Type: amino acids
; OTHER INFORMATION: Topology: Circular
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 2
; OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 6
; OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 8
; OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
US-10-196-937A-9
Query Match 48.1%; Score 26; DB 15; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 WLTIW 7
Db 1 WLWLW 5
RESULT 9
US-10-457-780-38
; Sequence 38, Application US/10457780
; Publication No. US20040137426A1
; GENERAL INFORMATION:
; APPLICANT: Serres, Pierre-Francois
; APPLICANT: Mosca, Joseph
; TITLE OF INVENTION: GP41 PEPTIDES AND METHODS BASED THEREON FOR INHIBITING HIV FUSION
; FILE REFERENCE: 118761
; CURRENT APPLICATION NUMBER: US/10/457,780
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/446,268
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/413,919
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/386,754
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 8
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US-10-367-654-227
; Sequence 227, Application US/10367654
; Publication No. US20040071723A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461032
; CURRENT APPLICATION NUMBER: US/10/367,654
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 10/171,734
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/636,295
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 227
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-654-227

Query Match          47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy      1 GYWLTIW 7
      |:|:|
Db      1 GWMVT-W 6

RESULT 15
US-10-367-668-227
; Sequence 227, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 227
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-227

Query Match          47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy      1 GYWLTIW 7
      |:|:|
Db      1 GWMVT-W 6

Search completed: January 3, 2005, 12:43:11
Job time : 140 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:22:35 ; Search time 38 Seconds
(without alignments)
20.256 Million cell updates/sec

Title: SEQ32

Perfect score: 54

Sequence: 1 gywlwiwg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 22 | 40.7 | 7 | 2 | PT0586 |
| 2 | 20 | 37.0 | 5 | 2 | JH0253 |
| 3 | 18 | 33.3 | 8 | 2 | J50315 |
| 4 | 17 | 31.5 | 4 | 2 | B53284 |
| 5 | 17 | 31.5 | 6 | 2 | PT0629 |
| 6 | 17 | 31.5 | 6 | 2 | PT0637 |
| 7 | 17 | 31.5 | 6 | 2 | A61068 |
| 8 | 17 | 31.5 | 7 | 2 | PT0628 |
| 9 | 17 | 31.5 | 7 | 2 | PT0642 |
| 10 | 17 | 31.5 | 7 | 2 | PT0722 |
| 11 | 17 | 31.5 | 7 | 2 | PT0728 |
| 12 | 17 | 31.5 | 7 | 2 | PX0008 |
| 13 | 17 | 31.5 | 7 | 2 | B48394 |
| 14 | 17 | 31.5 | 7 | 2 | PD0029 |
| 15 | 17 | 31.5 | 7 | 2 | S57274 |
| 16 | 17 | 31.5 | 7 | 2 | S33244 |
| 17 | 17 | 31.5 | 7 | 2 | S33245 |
| 18 | 17 | 31.5 | 7 | 2 | S33246 |
| 19 | 17 | 31.5 | 8 | 2 | PT0724 |
| 20 | 17 | 31.5 | 8 | 2 | J50316 |
| 21 | 17 | 31.5 | 8 | 2 | J50317 |
| 22 | 17 | 31.5 | 8 | 2 | J50318 |
| 23 | 17 | 31.5 | 8 | 2 | A31570 |
| 24 | 16 | 29.6 | 7 | 2 | S09652 |
| 25 | 15 | 27.8 | 6 | 2 | PT0532 |
| 26 | 15 | 27.8 | 6 | 2 | F41946 |
| 27 | 15 | 27.8 | 7 | 4 | A58725 |
| 28 | 15 | 27.8 | 8 | 2 | PH1618 |
| 29 | 15 | 27.8 | 8 | 2 | A59495 |

| | | | | | |
|----|----|------|---|---|--------|
| 30 | 15 | 27.8 | 8 | 2 | TI3818 |
| 31 | 14 | 25.9 | 6 | 2 | A31263 |
| 32 | 14 | 25.9 | 6 | 2 | B35640 |
| 33 | 14 | 25.9 | 6 | 2 | PT0519 |
| 34 | 14 | 25.9 | 7 | 2 | S21230 |
| 35 | 14 | 25.9 | 7 | 2 | PH1602 |
| 36 | 14 | 25.9 | 7 | 2 | S33567 |
| 37 | 13 | 24.1 | 4 | 2 | S09478 |
| 38 | 13 | 24.1 | 5 | 2 | A32516 |
| 39 | 13 | 24.1 | 6 | 2 | B34835 |
| 40 | 13 | 24.1 | 6 | 2 | B31263 |
| 41 | 13 | 24.1 | 6 | 2 | A61411 |
| 42 | 13 | 24.1 | 7 | 1 | A61324 |
| 43 | 13 | 24.1 | 7 | 2 | A60139 |
| 44 | 13 | 24.1 | 7 | 2 | S71870 |
| 45 | 13 | 24.1 | 7 | 2 | S36662 |

ALIGNMENTS

RESULT 1

PT0586

T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0586; PT0592

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0586

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-7 <PEE>

A:Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)

C:Keywords: T-cell receptor

Query Match 40.7%; Score 22; DB 2; Length 7;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TING 8

Db :|||

3 SING 6

RESULT 2

JH0253

gut pentapeptide - Japanese eel

C:Species: Anguilla japonica (Japanese eel)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995

C:Accession: JH0253

R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.

Biochem. Biophys. Res. Commun. 180, 828-832, 1991

A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.

A:Reference number: JH0253; MUID:92062113; PMID:1953755

A:Accession: JH0253

A:Molecule type: protein

A:Residues: 1-5 <UES>

A:Experimental source: gut

C:Comment: This peptide increased basal tone of the circular muscle of the esophagogastric

, and of the circular muscle of the gastro-intestinal junction.

Query Match 37.0%; Score 20; DB 2; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3

Db :|||

1 GFW 3

RESULT 3

JS0315
leucokinin V - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0315
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
A;Reference number: JS0315
A;Accession: JS0315
A;Molecule type: protein
A;Residues: 1-8 <HOL>

A;Cross-references: UNIPROT:P19987
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 33.3%; Score 18; DB 2; Length 8;

Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8

Db 1 GSGFSSWG 8

RESULT 4

B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and J
A;Reference number: A53284; MUID:91342695; PMID:1678859

A;Accession: B53284

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-4 <HAR>

A;Cross-references: GB:S60737; NID:G233916; PIDN:AAB19518.1; PID:G233918

A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:P:60738)

C;Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

Db 2 WG 3

RESULT 5

PT0629
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0629

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEE>

A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH

A;Accession: PT0528

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <PE2>

A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB
C;Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

Db 5 WG 6

RESULT 6

PT0637

T-cell receptor beta chain V-D-J region (111-1K) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0637

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0637

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

Db 5 WG 6

RESULT 7

A61068

locustakinin - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A61068

R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.

Regul. Pept. 37, 49-57, 1992

A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, prin

A;Reference number: A61068; MUID:92262851; PMID:1585017

A;Accession: A61068

A;Molecule type: protein

A;Residues: 1-6 <SCH>

A;Cross-references: UNIPROT:P41491

C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide

F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 31.5%; Score 17; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

Db 5 WG 6

RESULT 8

PT0628

T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0628

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0628
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 6 WG 7

RESULT 9

PT0642

T-cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0642

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0642

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-7 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 5 WG 6

RESULT 10

PT0722

T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0722

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0722

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-7 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 6 WG 7

RESULT 11

PT0728

T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0728
R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0728

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-7 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 5 WG 6

RESULT 12

PX0008

Glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)
N:Alternate names: UDP-glucuronyltransferase

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997
C:Accession: PX0008

R:Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A:Title: Purification and properties of a form of UDP-glucuronyltransferase from liver
A:Reference number: PX0008; MUID:89197852; PMID:3149280

A:Accession: PX0008

A:Molecule type: protein

A:Residues: 1-7 <YOK>

C:Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 LTIW 7
| : |
Db 3 LLVW 6

RESULT 13

B48394

major fat-globule membrane protein GP 55 - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)

C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: B48394

R:Mather, I.H.; Banghart, L.R.; Lane, W.S.

Biochem. Mol. Biol. Int. 29, 545-554, 1993

A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.

A:Reference number: A48394; MUID:93250576; PMID:8485470

A:Accession: B48394

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MAT>

A:Experimental source: milk

A:Note: sequence extracted from NCBI backbone (NCBIP:131444)

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 1 WG 2

```
RESULT 14
PD0029
pev-kinin 1 - penaeid shrimp (Penaeus vannamei) (fragment)
C;Species: Penaeus vannamei
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000
C;Accession: PD0029
R;Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devreese,
Biochem. Biophys. Res. Commun. 248, 406-411, 1998
A;Title: Identification of one tachykinin- and two kinin-related peptides in the brain of
A;Reference number: PD0027; MUID:98342103; PMID:9675150
A;Accession: PD0029
A;Molecule type: protein
A;Residues: 1-7 <NR>
C;Comment: This peptide belongs to myotropic neuropeptides.

Query Match      31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 WG 8
Db      6 WG 7

RESULT 15
S57274
triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)
C;Species: Psychrobacter immobilis
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57274
R;Arpigny, J.L.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1263, 103, 1995
A;Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the
A;Reference number: S57274; MUID:95359197; PMID:7632728
A;Accession: S57274
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-7 <ARP>
A;Cross-references: UNIPROT:Q02104; EMBL:X67712
C;Keywords: carboxylic ester hydrolase

Query Match      31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 WG 8
Db      1 WG 2

Search completed: January 3, 2005, 12:31:54
Job time : 39 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:14:40 ; Search time 189 Seconds
(without alignments)
24.354 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywltiwg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 835

Minimum DB seq length: 0
Maximum-DB-seq-length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|------------------------|
| 1 | 26 | 48.1 | 8 | 2 Q70Y57 | Q70Y57 fuerstia af |
| 2 | 26 | 48.1 | 8 | 2 CAD45547 | Cad45547 fuerstia |
| 3 | 21 | 38.9 | 8 | 2 AAB33374 | Aab33374 homo sapi |
| 4 | 20 | 37.0 | 7 | 2 Q8JB81 | Q8JB81 human immun |
| 5 | 19 | 35.2 | 5 | 1 UF01_MOUSE | UF01_MOUSE mus muscu |
| 6 | 18 | 33.3 | 8 | 1 LCK5_LEUMA | LCK5_LEUMA leucophaea |
| 7 | 18 | 33.3 | 8 | 1 PK4_PERAM | PK4_PERAM periplaneta |
| 8 | 18 | 33.3 | 8 | 1 LCK1_LOGMI | LCK1_LOGMI locusta mig |
| 9 | 17 | 31.5 | 6 | 1 LOK1_ACHFU | LOK1_ACHFU achatina fu |
| 10 | 17 | 31.5 | 7 | 1 WWA1_ACHFU | WWA1_ACHFU achatina fu |
| 11 | 17 | 31.5 | 7 | 1 WWA2_ACHFU | WWA2_ACHFU achatina fu |
| 12 | 17 | 31.5 | 7 | 1 WWA3_ACHFU | WWA3_ACHFU achatina fu |
| 13 | 17 | 31.5 | 7 | 2 O49223 | O49223 glycine max |
| 14 | 17 | 31.5 | 8 | 1 AC1_THUAL | AC1_THUAL thunnus alb |
| 15 | 17 | 31.5 | 8 | 1 LCK1_LEUMA | LCK1_LEUMA leucophaea |
| 16 | 17 | 31.5 | 8 | 1 LCK2_LEUMA | LCK2_LEUMA leucophaea |
| 17 | 17 | 31.5 | 8 | 1 LCK3_LEUMA | LCK3_LEUMA leucophaea |
| 18 | 17 | 31.5 | 8 | 1 LCK4_LEUMA | LCK4_LEUMA leucophaea |
| 19 | 17 | 31.5 | 8 | 1 LCK6_LEUMA | LCK6_LEUMA leucophaea |
| 20 | 17 | 31.5 | 8 | 1 LCK7_LEUMA | LCK7_LEUMA leucophaea |
| 21 | 17 | 31.5 | 8 | 1 LCK8_LEUMA | LCK8_LEUMA leucophaea |
| 22 | 17 | 31.5 | 8 | 1 PK1_PERAM | PK1_PERAM periplaneta |
| 23 | 17 | 31.5 | 8 | 1 PK2_PERAM | PK2_PERAM periplaneta |
| 24 | 17 | 31.5 | 8 | 1 PK3_PERAM | PK3_PERAM periplaneta |
| 25 | 17 | 31.5 | 8 | 1 PK5_PERAM | PK5_PERAM periplaneta |
| 26 | 17 | 31.5 | 8 | 1 RT34_BOVIN | RT34_BOVIN bos taurus |
| 27 | 17 | 31.5 | 8 | 2 Q70Y84 | Q70Y84 plectranthu |
| 28 | 17 | 31.5 | 8 | 2 Q7GEM6 | Q7GEM6 branchiosto |
| 29 | 17 | 31.5 | 8 | 2 Q6ZZ01 | Q6ZZ01 silene conl |
| 30 | 17 | 31.5 | 8 | 2 Q6ZZ02 | Q6ZZ02 lychnis cor |
| 31 | 17 | 31.5 | 8 | 2 CAD45500 | Cad45500 plectrant |

32 17 31.5 8 2 CAG24877 lychnis c
33 17 31.5 8 2 CAG24879 silene co
34 16 29.6 6 1 E101_LITRU P82096 litoria rub
35 16 29.6 7 2 Q9BRY4 Q9BRY4 homo sapien
36 16 29.6 8 2 O85406 O85406 coxiella bu
37 15 27.8 4 1 OCP3_OCTMI P88649 octopus min
38 15 27.8 8 1 VAM6_MOUSE P83853 mus musculu
39 15 27.8 8 2 Q715L5 Q715L5 varanus dum
40 15 27.8 8 2 Q94V88 Q94V88 varanus tri
41 15 27.8 8 2 Q94V91 Q94V91 varanus tim
42 15 27.8 8 2 Q94VA7 Q94VA7 varanus eal
43 15 27.8 8 2 Q94VB2 Q94VB2 varanus eal
44 15 27.8 8 2 Q94VB5 Q94VB5 varanus eal
45 15 27.8 8 2 Q94VC1 Q94VC1 varanus rud

ALIGNMENTS

RESULT 1

Q70Y57 PRELIMINARY; PRT; 8 AA.
AC Q70Y57;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=tps16;
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamnids; Lamiales; Lamiales; Nepetoideae; Ocimeae; Fuerstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -;
GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 48.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TIWG 8
Db 2 TIWG 5

RESULT 2

CAD45547 PRELIMINARY; PRT; 8 AA.
ID CAD45547
AC CAD45547;
DT 14-MAR-2004 (T-EMBLrel. 27, Created)
DT 14-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 14-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN RPS16.
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamnids; Lamiales; Lamiales; Nepetoideae; Ocimeae; Fuerstia.
OX NCBI_TaxID=204226;

```

RN SEQUENCE FROM N.A.
RP Paton A., Springate D.A., Sudde S., Ottieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RA "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL: AJ505427; CAD45547.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 48.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TIWG 8
Db ||||
2 TIWG 5

RESULT 3
AAB33374 PRELIMINARY; PRT; 8 AA.
AC AAB33374;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Collagen alpha 5(IV) chain (Fragment).
GN COL4A5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95156893; PubMed=7853788;
RA Nakazato H., Hattori S., Ushijima T., Matsuura T., Koitabashi Y.,
RA Takada T., Yoshioka K., Endo F., Matsuda I.;
RT "Mutations in the COL4A5 gene in Alport syndrome: a possible mutation
RT in primordial germ cells.";
RL Kidney Int. 46:1307-1314(1994).
DR EMBL: S75903; AAB33374.1; -.
FT NON_TER 1 1
FT NON_TER 8 AA; 933 MW; 7370437735BAB378 CRC64;

Query Match 38.9%; Score 21; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLTIW 7
Db |::|
2 WDSLW 6

RESULT 4
Q8JE81 PRELIMINARY; PRT; 7 AA.
ID Q8JE81
AC Q8JE81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22056123; PubMed=12060770;
RA Beerenwink N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;

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RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL: AF347267; AK32344.1; -.
FT NON_TER 1 1
FT NON_TER 7 AA; 885 MW; 76C37731A046C700 CRC64;
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 37.0%; Score 20; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIW 7
Db :||:
3 ITLW 6

RESULT 5
UF01_MOUSE STANDARD; PRT; 5 AA.
ID UF01_MOUSE
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON_TER 5 5
FT NON_TER 5 AA; 717 MW; 7364087043100000 CRC64;
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 35.2%; Score 19; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WLTIW 7
Db |::|
1 WIGRW 5

RESULT 6
LCK5_LEUMA STANDARD; PRT; 8 AA.
ID LCK5_LEUMA
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX TISSUE=Head; PubMed=2877794;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile

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CC activity of cockroach prothodum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; JS0315; JS0315.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 33.3%; Score 18; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GYWTWING 8
| : ||
Db 1 GSGFSSWG 8

RESULT 7
PK4_PERAM
ID PK4_PERAM STANDARD; PRT; 8 AA.
AC P82688;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kinin-4 (Pea-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
RT "Isolation and structural elucidation of eight kinins from the
RT reticocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=838.15; METHOD=Electrospray; RANGE=1-8;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the kinin family.
CC Amidation; Direct protein sequencing; Neuropeptide.
KW MOD RES 8 8 Glycine amide.
FT MOD RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 33.3%; Score 18; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GYWTWING 8
| : ||
Db 1 GAQFSSWG 8

RESULT 8
Q62721
ID Q62721 PRELIMINARY; PRT; 8 AA.
AC Q62721;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Prohibitin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher;
RX MEDLINE=95331633; PubMed=7607556;

RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT prohibitin-encoding genes.";
RL Gene 158:291-294(1995).
DR EMBL; U17178; AAA86692.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 1150 MW; BFD3237B05A41376 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WLTW 7
| : |
Db 2 WRSEW 6

RESULT 9
LOK1_LOCMI
ID LOK1_LOCMI STANDARD; PRT; 6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Locustakinin I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92252851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
CC -1- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Malpighian
CC tubules.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC PIR; A61068; A61068.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 6 6 Glycine amide.
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
| : |
Db 5 WG 6

RESULT 10
WWA1_ACHFU
ID WWA1_ACHFU STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.

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```
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayaashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -!- FUNCTION: Exhibits modulatory effects on the peripheral nervous
CC system. Inhibits activity on a central neuron.
DR PIR; S33245; S33245.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 Tryptophan amide.
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIW 7
Db ::|
4 MSVW 7

RESULT 11
WMA2 ACHFU STANDARD; PRT; 7 AA.
AC P35920;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wamide-2.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayaashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33246; S33246.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 Tryptophan amide.
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIW 7
Db ::|
4 MSVW 7

RESULT 12
WMA3 ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayaashi M., Nomoto K.;
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RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 Tryptophan amide.
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIW 7
Db ::|
4 MSVW 7

RESULT 13
O49223 PRELIMINARY; PRT; 7 AA.
AC O49223;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HMG-1-like protein (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RX MEDLINE=91367679; PubMed=1891369;
RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
RT with HMG-box proteins.";
RL Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF047050; AAC03556.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8
Db ||
2 WG 3

RESULT 14
ACI_THUAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
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RX MEDLINE=89326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
CC -!- FUNCTION: Inhibits angiotensin-converting enzyme.
DR PIR; A31570; A31570.
KW Direct protein sequencing; Metalloprotease inhibitor.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 6 WG 7

RESULT 15
LCK1 LEUMA STANDARD; PRT; 8 AA.
ID LCK1 LEUMA
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE. AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides from
RT Leucophaea maderae: members of a new family of Cephalomyototropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothorax (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 8
FT 8 Glycine amide.
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 31.5%; Score 17; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 6 WG 7

Search completed: January 3, 2005, 12:31:11
Job time : 190 secs

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